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(54) Title: MODULATORS OF TISSUE REGENERATION			
(57) Abstract Proteins which are upregulated in injured or regenerating tissues, as well as the DNA encoding these proteins, are disclosed, as well as therapeutic compositions and methods of treatment encompassing these compounds.			

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MODULATORS OF TISSUE REGENERATION**Related Applications**

This is a continuation-in-part of prior U.S. Provisionals S.N. 60/047,490 and S.N. 60/047,491, both filed May 23, 1997. The teachings of both earlier-filed Provisional patent applications are incorporated herein by reference.

10

Field of the Invention

The invention relates generally to gene expression products, including nucleic acids (e.g., RNAs) and polypeptides that are upregulated in injured or regenerating tissues. Further, the invention relates generally to cDNAs and other nucleic acids encoding polypeptides that are upregulated in injured or regenerating tissues.

15

Background of the Invention

The processes of tissue development during embryogenesis, and of tissue repair and/or regeneration following injury or insult are presently the topic of intense investigation. Both processes involve a dynamic remodeling of tissue architecture, which is triggered and mediated by numerous biological interactions, including cell-cell contact, cell-matrix contact, release of soluble biological response modifiers, synthesis of structural components, and many other changes in cell phenotype, including changes in gene expression. Many of the factors involved in tissue genesis and in the response to tissue insult remain unknown or poorly understood.

Several systems have been developed for modeling the events triggered by insult to particular tissues, and/or by particular types of insult. For example, several investigators have described events occurring in mammalian kidney tissue exposed to an ischemia-reperfusion insult. The kidney is able to repair damage to the proximal tubule epithelium through a complex series of events involving cell death, proliferation of surviving proximal tubule epithelial cells, formation of poorly differentiated regenerative epithelium over the

denuded basement membrane, and differentiation of the regenerative epithelium to form fully functional proximal tubule epithelial cells (Wallin et al., Lab. Invest. 66:474-484, 1992; Witzgall et al., Mol. Cell. Biol. 13:1933-1942, 1994; Ichimura et al., Am. J. Physiol. 269:F653-662, 1995; Thadhani et al., N. Engl. J. Med. 334:1448-1460, 1996). Growth
5 factors such as IGF, EGF, and HGF have been implicated in this process of repair, as has the endothelial cell adhesion molecule ICAM-1. However, the mechanisms by which the tubular epithelial cells are restored, either functionally and morphologically, remain poorly understood.

There accordingly is a need for an improved understanding of the biological
10 processes of tissue repair or regeneration. That is, there is a need to identify factors that are indicative of the initiation, development and resolution of normal wound healing or normal biological response to tissue insult. Similarly, there is a need to identify factors that are indicative of pathologies of abnormal responses to tissue insult or other stimulus, including autoimmune or other dysregulation pathologies, as well as pathologies associated with
15 abnormal tissue growth including neoplastic growth. Further, there is a need to identify factors that constitute appropriate targets for therapeutic intervention to stimulate, modulate, enhance, suppress or otherwise manipulate biological responses to tissue insult. Similarly, there is a need to identify factors that constitute appropriate targets for therapeutic intervention to manipulate abnormal or dysregulated responses to tissue insult
20 or other stimulus, including abnormal tissue growth associated with cancer (neoplasia) and, conversely, abnormal tissue quiescence associated with degenerative diseases.

Summary of the Invention

It is an object of this invention to identify factors that are indicative of the initiation, development and resolution of normal wound healing or normal biological response to
25 tissue insult. A specific object of this invention is to identify products (e.g., RNAs, cDNAs, polypeptides) of genes that are upregulated in the context of healing tissue, or in tissue exposed to insult or injury. A particular object is to identify products of genes that are upregulated in mammalian kidney tissue exposed to insult or injury, such as ischemia-

reperfusion injury. A second specific object of this invention is to identify products of genes that are upregulated in pathological conditions associated with abnormal responses to tissue insult or other stimulus, including autoimmune or other dysregulation pathologies, as well as pathologies associated with abnormal tissue growth including neoplastic growth.

- 5 A third specific object is to identify gene products that constitute appropriate targets for therapeutic intervention to stimulate, modulate, enhance, suppress or otherwise manipulate biological responses to tissue insult. A particular object is to identify gene products for therapeutic intervention to manipulate responses of mammalian kidney tissue to tissue injury, such as ischemia-reperfusion injury. A fourth specific object is to identify gene
- 10 products that constitute appropriate targets for therapeutic intervention to manipulate abnormal or dysregulated responses to tissue insult or other stimulus, including abnormal tissue growth associated with cancer (neoplasia) and, conversely, abnormal tissue quiescence associated with degenerative diseases. Thus, other particular objects of the invention include the identification of gene products as targets for therapeutic intervention
- 15 in the clinical management (including prophylaxis, maintenance and treatment) of kidney diseases, including diseases involving renal failure, and of cancers derived from or affecting renal tissue.

- The present invention rests on the discovery that the expression levels of numerous genes, including many genes heretofore unknown and/or uncharacterized, are upregulated
- 20 in mammalian kidney tissue that has been exposed to tissue insult or injury. More specifically, the present invention rests on the discovery of a novel class of Kidney Injury-associated Molecules (each member of the class is henceforth called a "KIM"). KIMs are polypeptides encoded by genes whose expression levels are upregulated in the mammalian kidney upon exposure to tissue injury, particularly after exposure to ischemia-reperfusion
- 25 injury. Any KIM is useful as an indicator of tissue status (preferably renal tissue status) or of a change therein (e.g, exposure to tissue injury, or the occurrence or stage of a tissue repair process). Any KIM further is useful as a target for therapeutic intervention to manipulate, whether by an agonist or an antagonist, a normal or abnormal tissue response to insult or other stimulus.

The invention accordingly provides, in a first aspect, purified and isolated nucleic acid molecules encoding all or a unique fragment of a KIM. In one embodiment, the present nucleic acids are RNAs. In another, they are DNA molecules, such as cDNAs. In another embodiment, the invention provides the complementary strands of nucleic acids encoding all or a unique fragment of a KIM. In another embodiment, the invention provides nucleic acids (preferably DNAs) that hybridize under low or, preferably, high stringency conditions to any of the foregoing nucleic acids. In still another embodiment, the invention provides nucleic acids (preferably DNAs) which, but for the degeneracy of the genetic code, would hybridize to any of the foregoing nucleic acids. In some embodiments, a nucleic acid encoding all or a unique fragment of a KIM is an engineered (recombinant) nucleic acid, optionally in operative association with an expression control element or other regulatory element. In other embodiments, a nucleic acid encoding all or a unique fragment of a KIM is an antisense nucleic acid sufficient, when internalized within a cell, to disrupt expression of a cellular KIM gene.

Specific novel KIMs (and unique fragments thereof) of the present invention are coded for by nucleic acids having the sequences disclosed herein in TABLE 1 and in the Sequence Listing. Other specific KIMs (and unique fragments thereof) are coded for by nucleic acids having sequences that are degenerate variants of any of the KIM sequences set forth in TABLE 1 and in the Sequence Listing. Still other specific KIMs (and fragments) are coded for by nucleic acids that are substantially similar to (homologous to) any of the KIM sequences in TABLE 1 and in the Sequence Listing. Such KIMs are defined herein as variants of the disclosed novel KIM sequences. In some embodiments, the present nucleic acid encodes a chimeric polypeptide comprising a novel KIM-encoding sequence (i.e., a sequence encoding part or all of a KIM) fused to a non-KIM sequence. Thus, the invention provides nucleic acids encoding novel KIM fusion proteins, non-limiting examples of which include KIM polypeptides fused to a secretable leader polypeptide, an immunoglobulin polypeptide, a binding pair partner (e.g., avidin, GST), a toxin or toxoid (e.g., ricin, tetanus), an enzyme (preferably one for which a detectable substrate is available, e.g., alkaline phosphatase, horseradish peroxidase, luciferase), or

other detectable polypeptide (e.g., green fluorescent protein). Additional specific KIMs (and unique fragments thereof) are coded for by nucleic acids referred to in TABLE 2. It is believed that, in most to all instances, these specific molecules have not heretofore been appreciated to be KIMs.

5 In a second aspect, the invention provides a vector having a KIM-encoding nucleic acid inserted therein. In some embodiments, the vector is a biologically functional plasmid or viral DNA vector. In other embodiments, the vector is a retroviral vector.

In a third aspect, the invention provides a prokaryotic or eukaryotic host cell comprising an internalized vector having a KIM-encoding nucleic acid insert. The present
10 host cell provides intracellular means for producing (synthesizing, folding, processing, or secreting) a KIM polypeptide of the present invention.

In a fourth aspect, the invention provides a process for the production of a KIM polypeptide. The present production process includes growing a host cell of the invention under culture conditions sufficient for the production of polypeptides of vector origin, and
15 recovering an expressed KIM polypeptide.

In a fifth aspect, the invention provides a purified and isolated novel KIM polypeptide, preferably substantially free of non-KIM polypeptides or proteins. In some embodiments, the present polypeptide is a full-length polypeptide, i.e., a polypeptide corresponding to the full-length open reading frame of a novel KIM-encoding cDNA. In
20 other embodiments, the present polypeptide is a unique fragment of the full-length polypeptide. Thus, specific novel KIM polypeptides (and unique fragments thereof) of the present invention are coded for by nucleic acids having the sequences disclosed herein in TABLE 1 and in the Sequence Listing. Other specific novel KIM polypeptides of the present invention are variants of the disclosed novel KIM sequences, including without
25 limitation splice variants, truncation variants, and substitution variants. In some embodiments, the invention provides a chimeric polypeptide comprising a novel KIM polypeptide fused (preferably via a peptide bond) to a non-KIM polypeptide. Thus, the invention provides novel KIM fusion proteins, exemplified by the above-mentioned fusion

constructs. Of course, the invention also provides conjugated or derivatized novel KIM polypeptides, including without limitation detectable conjugates, imageable conjugates, radiolabeled conjugates, and toxin conjugates. In still other embodiments, the invention provides chimeric polypeptides, fusion proteins and conjugates comprising a polypeptide
5 appreciated herein as being a KIM (see TABLE 2).

In a sixth aspect, the invention provides an antibody that binds selectively to a KIM polypeptide. Preferably, the antibody is a monoclonal antibody (or an engineered derivative thereof) produced by conventional means from a hybridoma derived from splenocytes of an animal immunized with a KIM polypeptide of the present invention. In
10 some embodiments, the present antibody is conjugated or derivatized with a detectable moiety, toxin, imageable compound or radionuclide.

In a seventh aspect, the invention provides a pharmaceutical composition comprising a therapeutically effective amount of a KIM nucleic acid (e.g., an antisense nucleic acid); a KIM vector; a KIM polypeptide; a KIM fusion protein; a KIM-binding
15 antibody (also referred to as an anti-KIM antibody), dispersed, dissolved or otherwise suspended in a physiologically acceptable carrier, vehicle, solvent or excipient.

In an eighth aspect, the invention provides methods and kits for detecting, either qualitatively or quantitatively, KIM expression and/or KIM polypeptide. As disclosed herein, KIMs are upregulated by exposure of mammalian kidney (renal) tissue to insult or
20 injury, particularly ischemia-reperfusion injury. Thus, any KIM (or combination or panel thereof) can be used as an indicator of tissue status (preferably renal tissue status), or of a change therein, including without limitation exposure to tissue injury, the occurrence or stage of an injury process, the occurrence or stage of a tissue repair or regeneration process, or the occurrence of an abnormal tissue response to injury or other stimulus, such as an
25 autoimmune response or an abnormal proliferative response (e.g., a neoplastic response).

In one embodiment, the invention provides a detection method and kit for diagnosis, prognosis, staging, or monitoring of renal injury or of renal disease or of the effectiveness of therapy therefor. Some specific embodiments involve detecting and/or

measuring the concentration of one or more KIM polypeptides in serum, urine, or urine sediment of an individual (a mammal, preferably a human) afflicted with or at risk of developing renal injury or an impairment of renal function. Some such embodiments involve the use of at least one KIM polypeptide, anti-KIM antibody or conjugate thereof as
5 elements of a reagent kit for immunoassay according to standard techniques. For present purposes, any KIM disclosed herein or identified as such herein can be used as a kit element, along with other elements for KIM detection. In other instances, such as where the detected KIM has biological or enzymatic activity, the kit can include reagents for detecting KIM activity, e.g., by enzyme assay. Other specific embodiments involve
10 detecting and/or measuring the level of expression of one or more KIM-encoding nucleic acids in renal cells in a kidney biopsy, or in cells shed into urine or urine sediment of an individual afflicted with or at risk of developing renal injury or an impairment of renal function. Some such embodiments involve the use of a nucleic acid (e.g., RNA or DNA) encoding a KIM polypeptide, or a unique fragment thereof, or a probe nucleic acid capable
15 of hybridizing to nucleic acid encoding a KIM, as elements of a reagent kit for hybridization assay according to standard techniques. As above, any KIM nucleic acid disclosed herein or appreciated herein as such can be used as a hybridization kit element, along with other reagents for detection of hybridized nucleic acids.

In another embodiment, the invention provides a method and kit for diagnosis,
20 prognosis, staging or monitoring of an abnormal response of renal tissue to tissue injury or other stimulus, including an autoimmune response or an abnormal proliferative response, such as neoplasia arising from or affecting renal tissue. Some specific embodiments involve detecting and/or measuring the concentration of one or more KIM polypeptides in serum, urine, or urine sediment of an individual (a mammal, preferably a human) afflicted
25 with or at risk of developing renal injury or an impairment of renal function. Some such embodiments involve the use of at least one KIM polypeptide, anti-KIM antibody or conjugate thereof as elements of a reagent kit for immunoassay according to standard techniques. For present purposes, any KIM disclosed herein or identified as such herein can be used as a kit element, along with other elements for KIM detection. In other instances,

such as where the detected KIM has biological or enzymatic activity, the kit can include reagents for detecting KIM activity, e.g., by enzyme assay. Other specific embodiments involve detecting and/or measuring the level of expression of one or more KIM-encoding nucleic acids in cells present in a kidney biopsy, or in cells shed into urine or urine sediment of an individual afflicted with or at risk of developing renal injury or an impairment of renal function. Some such embodiments involve the use of a nucleic acid (e.g., RNA or DNA) encoding a KIM polypeptide, or a unique fragment thereof, or a probe nucleic acid capable of hybridizing to nucleic acid encoding a KIM, as elements of a reagent kit for hybridization assay according to standard techniques. As above, any KIM nucleic acid disclosed herein or appreciated herein as such can be used as a hybridization kit element, along with other reagents for detection of hybridized nucleic acids.

In a ninth aspect, the invention provides a method and reagent for imaging tissues, either *in vitro* or *in vivo*. In particular, the invention provides a method and reagent for imaging the presence, extent or severity of kidney injury or of kidney tissue repair or regeneration. Similarly, the invention provides a method and reagent for imaging the presence, extent, severity or stage of an abnormal response to tissue injury or other stimulus, such as autoimmunity or neoplasia, particularly neoplasia arising from or affecting renal tissue. The present invention also provides a method for targetting an imageable compound to cells or tissue expressing or producing a KIM. The present method involves the step of contacting cells or tissue with a detectable (e.g., imageable) KIM-binding reagent, which in some embodiments is an anti-KIM antibody or conjugate thereof, or a KIM fusion protein. In other embodiments, the detectable KIM-binding reagent is a nucleic acid of the invention (e.g., a probe or antisense nucleic acid) labeled with a radionuclide or other imageable compound. According to the present method, cells expressing or producing a KIM are visualized (imaged) by detecting the presence and/or location of an accumulation of the KIM-binding reagent. For imaging *in vivo*, the KIM-binding reagent is administered, by any appropriate route, to an individual (a mammal, preferably a human) suspected of harboring an imageable locus of KIM expression and/or production. Without being limited hereby, it is believed that the present method can be

used to detect the presence and/or location of a tissue mass (e.g., a tumor) abnormally producing or expressing a KIM.

In a tenth aspect, the invention provides methods for treating an individual (a mammal, preferably a human) afflicted with or at risk of developing a disease or condition contributed to or associated with a dysfunction or dysregulation of a KIM gene or protein. Further, the invention provides methods for treating an individual afflicted with or at risk of developing a disease or condition beneficially affected by therapeutic administration of a KIM protein. The present methods involve the step of administering to the individual a therapeutically effective amount of a KIM polypeptide, variant or fusion protein thereof, or, conversely, of an anti-KIM antibody. It is expected that such compounds will be useful in therapeutic methods which manipulate, e.g., stimulate or inhibit, biological responses that are dependent on KIM function.

In an eleventh aspect, the invention provides a method for inhibiting the growth of KIM-expressing tumor cells, involving the step of contacting the cells with an anti-KIM antibody, conjugated to a toxin or radionuclide. In an alternative embodiment, the method involves the step of contacting the cells with an antisense KIM nucleic acid that is sufficient to suppress or disrupt expression of a KIM gene in the tumor cells.

In a twelfth aspect, the invention provides a method of gene therapy. The present method involves the administration of a vector capable of directing the production of a KIM, to an individual afflicted with or at risk of a renal disorder, disease or injury. As a result of the present method, growth of new tissue, preferably renal tissue, is stimulated, or survival of existing tissue, preferably renal tissue, is promoted.

The foregoing and other objects, features, aspects and advantages of the present invention, as well as the invention itself, will be more fully understood from the following description of preferred embodiments.

Detailed Description of the Invention

The discovery, reported herein, of a novel class of Kidney Injury-related Molecules (KIMs) was made by analyzing differences in mRNA expression between normal adult mammalian kidneys, and kidneys in the process of regenerating following exposure to tissue insult (specifically, to ischemia-reperfusion injury). Two established techniques were used for this purpose: representational difference analysis (RDA), and suppression subtractive hybridization (SSH). Both techniques were used to assess cDNAs isolated from various timepoints, e.g., 48 hours, after the onset of ischemia. In these studies, the normal adult kidney material was isolated from sham-operated subjects. Both techniques resulted in the depletion of cDNAs which are common to both postischemic and to normal kidney samples, leaving a pool of cDNAs which are significantly expressed only in injured or regenerating kidney tissue. This pool likely contains cDNAs corresponding to genes that encode proteins involved in the injury process, *and* proteins involved in tissue repair or regeneration processes. Therefore, cDNAs isolated from the pool likely encode parts or all of proteins likely to be therapeutically beneficial for treatment or prophylaxis of tissue injury, especially renal injury. Several cDNA clones have been obtained, sequenced and characterized.

Selected Definitions

A "KIM protein", herein used synonymously with "KIM", is any protein or polypeptide encoded by mRNA which is selectively upregulated following injury to a kidney. One group of KIM proteins of interest includes those coded for by mRNA which is selectively upregulated at any time within one week following any insult which results in injury to renal tissue. Examples of times at which such upregulation might be identified include 10 hours, 24 hours, 48 hours or 96 hours following an insult. Examples of tissue insults include toxin exposure, hypoxia, hyperoxia, hemodynamic disruption, ischemia, reperfusion, or mechanical compression. Many different types of proteins fall within the KIM class, including cell surface proteins (e.g., ligands or counter-receptors involved in cell-cell or cell-matrix interactions), secreted proteins (e.g., diffusable biological response modifiers, such as growth factors, differentiation factors, survival factors and the like),

intracellular proteins (e.g., elements of a signalling pathway), and nuclear proteins (e.g., transcription factors).

A "KIM ligand" is any molecule which noncovalently and specifically binds to a KIM protein. Such a ligand can be a protein, peptide, steroid, antibody, amino acid
5 derivative, or other type molecule, in any form, including naturally-occurring, recombinantly produced, or otherwise synthetic. A KIM ligand can be in any form, including soluble, membrane-bound, or part of a fusion construct with immunoglobulin, fatty acid, or other moieties. The KIM ligand may be an integrin. A membrane-bound KIM ligand can act as a receptor which, when bound to or associated with KIM, triggers a
10 cellular response. In some interactions, a KIM may associate with a plurality of KIM ligands, or may associate with a KIM ligand as part of a complex with one or more other molecules or cofactors. In a situation where both the KIM and the KIM ligand are bound to cell membranes, the KIM may associate and react with KIM ligand which is bound to the same cell as the KIM, or it may associate and react with KIM ligand be bound to a
15 second cell. Where the KIM ligation occurs between molecules bound to different cells, the two cells may be the same or different with respect to cellular type or origin, phenotypic or metabolic condition, or type or degree of cellular response (e.g., growth, differentiation or apoptosis) to a given stimulus. "KIM ligation" refers to the contact and binding of KIM with a KIM ligand.

20 A "unique fragment" of a nucleic acid means any fragment of sufficient length to have a sequence likely to be substantially unique in a mammalian genome. Thus, a unique fragment generally means an oligonucleotide at least 16 nucleotide bases in length. Similarly, a "unique fragment" of a polypeptide means any fragment of sufficient length to have an amino acid sequence likely to be substantially unique to a given mammalian
25 protein, such as a KIM. Thus, a unique peptide fragment generally means a peptide at least 7 amino acids in length.

A "KIM variant" means a KIM whose sequence differs from a sequence disclosed herein by the presence of one or more internal or terminal insertions, deletions or substitutions of a nucleotide (when referring to KIM nucleic acids) or of an amino acid

(when referring to KIM polypeptides). Preferably, the KIM variant is "substantially similar" to the corresponding disclosed KIM, or to a unique fragment thereof. That is, the KIM variant is "homologous" to the corresponding disclosed KIM. "Substantially similar" or "homologous" variants are structurally similar to the corresponding disclosed KIM. Further, "substantially similar" or "homologous" variants have sufficient functional similarity to the corresponding disclosed KIM that they share one or more of the KIM's biological properties or functions (e.g., binding to a receptor or ligand, triggering of biological responses, transport of a metabolite, catalysis of a substrate, or the like). A KIM variant can be naturally occurring or synthesized or produced by routine techniques, such as molecular engineering techniques.

By "alignment of sequences" is meant the positioning of one sequence, either nucleotide or amino acid, with that of another, to allow a comparison of the sequence of relevant portions of one with that of the other. Generally, sequences are aligned using the GAP and BESTFIT programs, which are based on the teachings of Needleman et al. (J. Mol. Biol. 48:443-453, 1970), Smith et al. (Adv. Appl. Math. 2:482-489, 1981), and Rechid et al. (CABIOS 5:107-113, 1989). Generally, when a homologous variant of a KIM is aligned with the corresponding KIM polypeptide, it will share amino acids that contribute to the KIM's three dimensional structure, such as cysteine residues. Although the relative positions of cysteine residues is generally conserved in the variant sequence, homologous or functionally equivalent sequences can include functionally equivalent arrangements of the cysteines, including arrangements comprising amino acid insertions or deletions which alter the linear arrangement of the cysteines, but do not materially impair their relationship or ability to form disulfide bonds in the folded structure of the KIM protein. Therefore, minor internal gaps and amino acid insertions, such as occur in splice variants, are ignored when aligning sequences herein.

"Sequence homology", "percent (%) homology", "sequence similarity" and "percent (%) similarity" are used interchangeably herein, and refer to the *sum* of the percentage of residues (whether nucleotides or amino acids) that are, when aligned with a reference sequence, the same as the corresponding reference residues, *and* those that are,

when aligned, conservative substitutions for the corresponding reference residues.

“Sequence identity” and “percent (%) identity” also are used interchangeably herein, and refer to the percentage of residues (whether nucleotides or amino acids) that are, when aligned with a reference sequence, the same as the corresponding reference residues. Both
5 sets of terms are used according to their definitions in Altschul et al. (1990), J. Mol. Biol. 215:403-410 and in the Basic Local Alignment Search Tool (BLAST) algorithm described therein. For present purposes, the algorithm gap weight is set at 3.0 and the length weight is set at 0.1.

“Hybridization” means the formation of a duplex nucleic acid molecule, in which
10 nucleotide bases of a first polynucleotide strand bind noncovalently with cognate nucleotide bases of a second polynucleotide strand. Generally, such noncovalent binding occurs in DNA only between adenosine (A) and thymidine (T) bases, and guanosine (G) and cytosine (C) bases. In RNA, binding occurs only between A and uracil (U), and G and C. The apposition of non-cognate bases in a duplex nucleic acid molecule, e.g., A with C,
15 is termed a “mismatch” pairing. Under high stringency hybridization conditions, mismatches occur rarely in a given duplex nucleic acid molecule. Low stringency conditions permit the occurrence of some mismatches. Exemplary conditions which promote DNA hybridization, termed “hybridization conditions”, include 6.0X sodium chloride/sodium citrate (SSC) at about 45°C, followed by a wash of 2.0X SSC at 50°C.
20 The salt concentration in the wash step can be selected from a low stringency wash of about 2.0X SSC at 50°C, to a high stringency wash of about 0.2X SSC at 50°C. In addition, the temperature in the wash step can be selected from a low stringency wash at room temperature, about 22°C, to a high stringency wash at about 65°C.

A “KIM agonist” is a molecule which can specifically trigger a cellular response
25 normally triggered by the interaction of KIM with a KIM ligand. A KIM agonist can be a KIM variant, or a specific antibody to KIM, or a soluble form of the KIM ligand.

A “KIM antagonist” is a molecule which can specifically associate with a KIM ligand or a KIM, thereby blocking or otherwise inhibiting KIM binding to the KIM ligand. The antagonist binding blocks or inhibits cellular responses which would otherwise be

triggered by ligation of the KIM ligand with KIM or with a KIM agonist. Examples of KIM antagonists include certain KIM variants, KIM fusion proteins and specific antibodies to a KIM ligand or KIM.

5 "Isolated" refers to a condition in which a nucleic acid or polypeptide of the present invention is essentially free of other nucleic acids, polypeptides, or of other contaminants with which it might normally be found in nature, and as such exists in a form not found in nature.

"Substantially pure" refers to a condition in which a nucleic acid or polypeptide of the present invention is separated from other nucleic acids, polypeptides, or other
10 contaminants, particularly naturally occurring contaminants, that interfere with the ability to detect, visualize or isolate the the nucleic acid or polypeptide of the invention, or that interfere with a biological function or property thereof. A substantially pure nucleic acid or polypeptide of the invention is not generally found in nature.

A "chemical derivative" of another molecule contains one or more additional
15 chemical or biochemical moieties not found naturally in association with the molecule. Such moieties may improve the molecule's solubility, absorption, biological half life, etc. The moieties may alternatively decrease the toxicity of the molecule, eliminate or attenuate any undesirable side effect of the molecule, etc. Moieties capable of mediating such effects are disclosed, for example, in Remington's Pharmaceutical Sciences, 16th ed., Mack
20 Publishing Co., Easton, Penn. (1980).

Other terms used herein, including "antisense DNA", "antisense probe", "cloning", "cDNA", "cDNA library", "DNA polymorphism", "expression", "gene", "hybridoma", "plasmid", "probe", "labeled", "recombinant", "host cells", "transformed", "transfected", "vector", and the like are used in the sense of their art-recognized meanings in the fields of
25 cell biology, cell culture, molecular biology, transgenic biology, microbiology, recombinant DNA or genetic engineering, and immunology. Such meanings are determined by consultation of one or more of the following widely available texts: Molecular Cloning, A Laboratory Manual, 2nd Ed. (Sambrook, Fritsch and Maniatis, eds.),

- Cold Spring Harbor Laboratory Press, 1989; DNA Cloning, Volumes I and II (Glover, ed.), 1985; Oligonucleotide Synthesis (Gait, ed.), 1984; U.S. Patent 4,683,195, Mullis et al., invs.; Nucleic Acid Hybridization (Hames & Higgins, eds.), 1984; Transcription and Translation (Hames & Higgins, eds.), 1984; Culture of Animal Cells (Freshney), Alan R. Liss, publ., 1987; Immobilized Cells and Enzymes (IRL Press), 1986; A Practical Guide to Molecular Cloning (Perbal), 1984; Current Protocols in Molecular Biology, Wiley & Sons, publ., 1989; Methods in Enzymology, Academic Press, New York NY (especially Volumes 154 and 155); Gene Transfer Vectors for Mammalian Cells (Miller and Calos, eds.), Cold Spring Harbor Laboratory Press, 1987; Immunochemical Methods in Cell and Molecular Biology (Mayer and Walker, eds.), Academic Press, London, 1987; Handbook of Experimental Immunology, Volumes I-IV (Weir and Blackwell, eds.), 1986; and, Manipulating the Mouse Embryo, Cold Spring Harbor Laboratory Press, 1986.

Compounds of the Invention

- Specific, novel KIMs discovered through RDA or SSH techniques are set forth below in TABLE 1 and in the Sequence Listing. TABLE 1 lists KIMs for which potential full length (PFL) cDNA clones were obtained. Also shown are the predicted polypeptide sequences encoded in the open reading frames (ORFs) of many of the newly discovered KIMs. In addition, TABLE 1 provides, where relevant, the subtracted amplified clone (SAC) designations and the PFL location(s) of partial sequences, many of which were reported in prior U.S. Provisional S.N. 60/047,490 and 60/047,491.

TABLE 1

SEQ. NO.	PFL	CLONE DESIGNATION	OPEN READING FRAME (OFR)	
			LOCATION	SEQ. ID #
# 3	HW011	HW011		
# 4	HW012	HW012	39..671	# 5
# 6	HW013	HW013		
# 7	HW014	HW014rev	175..804	# 8
# 9	HW015	HW15	11..2176	# 10
# 12	HW017	SAC_24091		
# 13	HW018 HW101	SAC_23880	86..1102	# 14
# 16	HW033	SAC_23901		
# 17	HW034	SAC_23897	91..837 3101..4162	# 18 # 19
# 20	HW035 HW112	SAC_24468		
# 21	HW036	SAC_24406		
# 22	HW037 HW102	SAC_24354	280..1422	
# 26	HW040	SAC_24520	481..2433	# 27
# 28	HW041	SAC_24317		
# 29	HW042 HW113	SAC_24017	8..889	# 30
# 31	HW043	SAC_24533	8..634	# 32
# 33	HW044	SAC_24216	24..1100	# 34
# 35	HW045	SAC_24028	9..1628	# 36
# 37	HW046	SAC_24036	9..1160	# 38
# 39	HW047	SAC_23915	8..511	# 40
# 42	HW050 HW109	SAC_24644	7..1326	# 43
# 44	HW051	SAC_24170	114..1505	# 45
# 46	HW052	SAC_24882	247..765	# 47
# 49	HW055	SAC_24449	214..1329	# 50
# 51	HW056	SAC_24326	8..523	# 52
# 53	HW057	SAC_23926	7..1023	# 54
# 55	HW059	SAC_24457	9..1271	# 56
# 57	HW061	SAC_24029	7..1422	# 58
# 61	HW069	SAC_24477	1360..1893	# 62
# 64	HW073	SAC_24456	9..1223	# 65
# 66	HW074	SAC_24464	7..300	# 67
# 68	HW075 HW117	SAC_24466		
# 69	HW076	SAC_24409		
# 71	HW080	SAC_24033		
# 72	HW082	SAC_24469	150..569	# 73
# 75	HW084	SAC_24854		
# 76	HW088	SAC_24336	9..686	# 77
# 78	HW089	SAC_24461	8..1006	# 79

TABLE 1, continued

SEQ. NO.	PFL	CLONE DESIGNATION	OPEN READING FRAME (OFR)	
			LOCATION	SEQ. ID #
# 80	HW090 HW118	SAC_24197	335 . 937	# 81
# 82	HW092	SAC_24320		
# 83	HW093	SAC_24538	8 . . 1357	# 84
# 85	HW094	SAC_23896	255 . . 1238	# 86
# 87	HW095	SAC_23802	7 . . 876	# 88
# 89	HW096	NONE	295 . . 1302	# 90

Additional KIMs, which are believed to be related to (e.g., substantially similar to) known molecules also were obtained through RDA or SSH techniques, and are set forth in

5 TABLE 2 and in the Sequence Listing. It is believed that few to none of these molecules were previously appreciated to be KIMs, i.e., to have relevance to tissue injury or repair processes, particularly in the kidney. TABLE 2 lists these KIMs along with their clone designations. Partial sequences of some of the cDNA clones listed below were also set forth in the priority document. Also shown are the name(s) and GENBANK accession

10 numbers of the known genes to which these KIMs may be related.

TABLE 2

SEQ ID #	DESIGNATION	RELATED GENE	Accession #
92	23798	Rat alpha 1A (1D) adrenergic receptor	M60654
93	23800	Rat N27	V30789
94	23801	Rat alpha-2mu globulin-related protein	X13295
95	23833	Rat contrapsin-like protease inhibitor related protein	X16359
96	23836	Rat Fit-1	V04319
97	23853	Rat tumor-associated antigen (pE4)	L12025
98	23906	Rat sulfated glycoprotein 2	X13231
99	23907	Mouse secreted protein (p85)	L33416
100	23916	Human Differentiation-dependent A4 protein	L09604

TABLE 2, continued

SEQ ID #	DESIGNATION	RELATED GENE	Accession #
101	23922	Rat manganese-containing superoxide dismutase	Y00497
102	24030	Rat heme oxygenase	J02722
103	24078	Rat tissue inhibitor of metalloproteinase 1 (TIMP1)	U16022
104	24105	Rat alpha 2- macroglobulin	J02635
105	24140	Rat Cathepsin D	X54467
106	24142	Rat lysozyme	L12458
107	24192	Mouse MAMA mRNA	X67809
108	24296	Rat transketolase	U09256
109	24445	Rat heat stable antigen CD24/ Elongation factor 1	Z11531
110	24527	Cathepsin L	S85184
111	24540	Mouse endothelial monocyte-activating polypeptide 1	U41341
112	24623	Rat spleen thymosin beta4	K01334
1	HW010	Human semaphorin (CD100)	U60800
11	HW016	Mouse ribonucleotide reductase M2 subunit	M14223
15	HW032	Human S100C	D49355
24	HW038	Human splicing factor SF3a120	X85237
25	HW039	Annexin 11	M82802
41	HW049	Mouse u22 snoRNA host gene (UHG)	U40654
48	HW054	Rat myelin oligodendrocyte protein (MOG)	M99485
59	HW062	Mouse proliferation-associated protein 1	U43918
60	HW066	Human cleavage stimulation factor 50kd subunit	L02547
63	HW070	Human BRCA2 region mRNA sequence CG037	U50523

TABLE 2, continued

SEQ ID #	DESIGNATION	RELATED GENE	Accession #
70	HW078	Human G protein gamma-10 subunit	P50151
74	HW083	Rat ins-1 winged helix	P97691
91	HW097	Human Na ⁺ channel 2	U78181

Any of the foregoing KIM cDNAs can be inserted into a vector, liposome or other carrier vehicle for internalization and production in a host cell. Furthermore, the invention encompasses derivatives and variants of each of the foregoing KIMs as listed in TABLES 1 and 2.

One embodiment of the invention provides soluble variants of a KIM protein that is usually synthesized as a membrane associated protein. Soluble variants lack at least a portion of the transmembrane or intra-membrane section of a native KIM protein. In some examples, the soluble variant lacks the entire transmembrane or intra-membrane section of a native KIM protein. Soluble variants include fusion proteins which encompass derivatives of KIM proteins that lack at least a portion of the transmembrane or intra-membrane section of a native KIM protein. All types of KIM fusion proteins are included, particularly those which incorporate his-tag, Ig-tag, and myc-tag forms of the molecule. These KIM fusions may have characteristics which are therapeutically advantageous, such as the increased half-life conferred by the Ig-tag. Also included are fusion proteins which incorporate portions of selected domains of the KIM protein.

Variants can differ from a naturally occurring KIM protein in amino acid sequence or in ways that do not involve sequence, or both. Variants in amino acid sequence are produced when one or more amino acids in naturally occurring KIM protein is substituted with a different natural amino acid, an amino acid derivative or non-natural amino acid. Particularly preferred substitution variants include naturally occurring KIM proteins, or biologically active unique fragments thereof, whose sequences differ from the wild type sequence by one or more conservative amino acid substitutions, which typically have minimal influence on the secondary structure and hydrophobic nature of the protein or

peptide. Conservative substitutions typically include the substitution of one amino acid for another with similar characteristics, such as substitutions within the following groups: valine, glycine; glycine, alanine; valine, isoleucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine.

- 5 Other conservative substitutions are those which meet the criteria for an "accepted point mutation" as defined in the Atlas of Protein Sequence and Structure (Dayhoff et al., eds.), 1978. See also PCT publication no. WO97/44460.

Substitution variants can also have sequences which differ by one or more non-conservative amino acid substitutions, provided however that the substitution does not
10 abolish the native KIM protein's biological activity, ligand- or receptor-binding characteristics, or other functional property of interest. Exemplary non-conservative substitutions are those in which: (i) a hydrophilic residue, e.g., serine or threonine, is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, or alanine; (ii) a cysteine residue is substituted for (or by) any other residue; (iii) a residue
15 having an electropositive side chain, e.g., lysine, arginine or histidine, is substituted for (or by) a residue having an electronegative charge, e.g., glutamic acid or aspartic acid; or (iv) a residue having a bulky side chain, e.g., phenylalanine, is substituted for (or by) one not having such a side chain, e.g., glycine.

Other KIM variants of this invention include truncation variants (comprising at
20 least a unique fragment of the corresponding KIM), insertion variants, and splice variants.

Other KIM variants within the invention are those with modifications which increase polypeptide stability. Such variants can contain, for example, one or more non-peptide bonds (which replace the peptide bonds) in the peptide sequence. Also included are: variants that include residues other than naturally occurring L-amino acids, such as D-
25 amino acids or non-naturally occurring or synthetic amino acids such as beta or gamma amino acids and cyclic variants. Incorporation of D- instead of L-amino acids into the polypeptide may increase its resistance to proteases. See, e.g., U.S. Patent 5,219,990.

KIM variants can be naturally-occurring, or produced through synthetic or molecular engineering techniques. Those of skill in the art will understand and appreciate that an engineered KIM variant can provide advantageous properties, e.g., in facilitating purification, improving stability, modulating a biological function, or the like. Thus, in some instances, a KIM variant will be desired that lacks a glycosylation site, or that has decreased aggregation potential due to elimination of a hydrophobic surface, or that has improved folding efficiency due to elimination of a cysteine residue, or the like.

In general, KIM variants have at least fifty (50) % amino acid sequence homology or similarity with the corresponding KIM protein. Preferably, the variants have at least sixty-five (65) % sequence similarity, more preferably at least eighty (80) % similarity with the corresponding KIM protein. Still more preferably, the sequence similarity is at least ninety (90) %, or most preferably, at least ninety-five (95) %. Other preferred KIM variants are those which 1) share at least forty (40) % similarity to the corresponding KIM protein, and 2) share at least eighty (80) % of aligned cysteine residues with the corresponding KIM protein.

Just as it is possible to replace substituents of the amino acid backbone or scaffold, it is also possible to replace, modify or add non-amino acid moieties to the scaffold. Such moieties can occur naturally in a given KIM as a result of post-translational processing, including acetylation, methylation, phosphorylation, carboxylation or glycosylation. As desired, such moieties can be removed or added by conventional synthetic or biochemical techniques. Further, non-natural moieties can be added to produce a derivative of a KIM or KIM variant of this invention. For example, polyethylene glycol (PEG) can be linked to a KIM to improve its stability or pharmacokinetic properties.

As will be readily appreciated, anti-KIM and anti-KIM variant antibodies can be produced by conventional techniques. Specifically contemplated are polyclonal and monoclonal antibodies, including antigen-binding fragments thereof and engineered derivatives thereof. Antigen-binding fragments of intact antibodies include complete Fab fragments, F(ab')₂ compounds, V_H regions, and F_V regions. Engineered derivatives of antibodies of the invention include single chain antibodies (see, e.g., WO 96/23071), as

well as human, humanized, primatized, or chimeric antibodies (see, e.g., PCT/US 95/16709). Engineered derivatives of the present antibodies are produced, generally, using standard recombinant DNA techniques (Winter and Milstein, Nature 349: 293-99, 1991). These include "chimeric" antibodies, in which the antigen binding domain from an animal
5 antibody is linked to a human constant domain. In this instance, an antibody with the desired KIM-binding selectivity is derived initially from a nonhuman mammal (e.g., a mouse, rat or hamster), and subjected to recombinant DNA manipulation to replace all or part of the hinge and constant regions of the heavy chain and/or the constant region of the light chain, with corresponding regions from a human immunoglobulin light chain or heavy
10 chain. (See, e.g., Cabilly et al., United States Pat. No. 4,816,567; Morrison et al., Proc. Natl. Acad. Sci. 81: 6851-55, 1984). Chimeric antibodies reduce the immunogenic responses elicited by animal antibodies when used in human clinical treatments.

In addition, recombinant "humanized" antibodies can be synthesized. Humanized antibodies are antibodies initially derived from a nonhuman mammal in which recombinant
15 DNA technology has been used to substitute some or all of the amino acids not required for antigen binding with amino acids from corresponding regions of a human immunoglobulin light or heavy chain. That is, they are chimeras comprising mostly human immunoglobulin sequences into which the regions responsible for specific antigen-binding have been inserted (see, e.g., PCT patent application WO 94/04679). Animals are immunized with
20 the desired antigen, the corresponding antibodies are isolated and the portion of the variable region sequences responsible for specific antigen binding are removed. The animal-derived antigen binding regions are then cloned into the appropriate position of the human antibody genes in which the antigen binding regions have been deleted. Humanized antibodies minimize the use of heterologous (inter-species) sequences in antibodies for use
25 in human therapies, and are less likely to elicit unwanted immune responses. Primatized antibodies can be produced similarly.

If desired, fully human antibodies with KIM-binding specificity which can be produced in nonhuman animals, such as transgenic animals harboring one or more human

immunoglobulin transgenes. Such animals may be used as a source for splenocytes for producing hybridomas, as is described in U.S. 5,569,825.

Identification of Specific KIMs of the Invention

To assess the dynamic biological processes of response to injury and tissue repair, a kidney ischemia-reperfusion model, which simulates acute renal failure, was employed. The results of studies in this model system now have been published, and appear in Ichimura et al. (1998), J. Biol. Chem. 273:4135-4142, the teachings of which are incorporated by reference herein. In this model, the kidney has the capacity for cell renewal (both structurally and functionally) after injury to tubular epithelial cells. The nephron is damaged functionally by an ischemic reperfusion injury that results in regional areas of proximal tubule cell death. During the repair process, the kidney proximal tubule epithelium undergoes a complex series of events including (1) cell death and cast formation in the tubule lumen (casts are aggregates of dead, semiviable and viable cells, as well as of cell debris); (2) proliferation of surviving proximal tubule epithelial cells; (3) formation of a poorly differentiated regenerative epithelium over the denuded basement membrane (this simplified epithelium expresses vimentin, a mesenchymal marker); and (4) differentiation of the regenerative epithelium to form fully functional proximal tubule epithelial cells. Gene expression analysis of the kidney at various timepoints following the onset of ischemia revealed the upregulation of many KIMs anticipated to be involved in the injury and repair/regeneration processes.

1. Generation of ischemic and normal rat adult kidneys

Ischemic injured rat kidneys are generated as described by Witzgall et al. (J. Clin Invest. 93: 2175-2188, 1994). Briefly, the renal artery and vein from one kidney of an adult Sprague-Dawley rat are clamped for 40 minutes and then reperused. Injured kidneys are harvested from the rats at 24 hours and at 48 hours after reperfusion. Kidneys from sham-operated, normal adult Sprague-Dawley rats are also harvested.

2. mRNA isolation

Post-ischemic rat kidneys are prepared as described by Witzgall et al. (J. Clin. Invest. 93: 2175-2188, 1994). Briefly, the renal artery and vein of the left kidney of an adult Sprague Dawley rat are clamped for 40 minutes and then reperfused. The ischemic kidneys are removed from rats either 24 hours or 48 hours after reperfusion. Normal rat kidneys are used as controls.

Total RNA is isolated with Trizol reagent (BRL catalog No. 1559-026). The kidney capsules are removed, then the kidneys are rinsed in PBS and immediately homogenized in Trizol solution. In some instances, the kidney is chopped into several pieces in PBS, frozen quickly in liquid nitrogen and kept at -70°C until it is processed for total RNA isolation.

The mRNA is purified from total RNA according to the manufacturer's instructions, using an mRNA purification kit (Pharmacia, Catalog No. 27-9258-02).

3(i). Representational difference analysis (RDA) method to clone short-fragment cDNAs up-regulated by ischemia

The RDA method of Hubank and Schatz (Nucleic Acid Research 22:5640-48, 1994) is performed as described, with modifications as follow. Double-stranded cDNA is synthesized using the Superscript Choice® system (BRL Catalog No. 18090), from mRNA isolated from rat kidney either 24 hours or 48 hours post-ischemia as a tester and normal rat kidney as a driver. The tester and driver cDNA is digested with DpnII and ligated to R-Bgl-12/24 oligonucleotides. The adapter-ligated cDNA is amplified by PCR, and the PCR product is digested with DpnII to remove the oligonucleotides. The tester cDNA is ligated to J-Bgl-12-24 oligonucleotides.

Full length cDNA clones for Kim-1 and NMB contained in a plasmid vector are provided by T. Ichimura. They are digested with Sau3A1, purified and used as quenching reagents. cDNA fragments, 2-3 containing a fragment of annexin II, and 3-8 containing a fragment of alpha 2 macroglobulin (both provided by T. Ichimura) are amplified by PCR with R-Bgl-24 primer, digested with DpnII to remove the oligonucleotides and used as quenching reagents. Tester cDNA is hybridized to an excess driver cDNA including the four quenching reagents described above. After mung bean nuclease digestion.

hybridization mixture is amplified by PCR to enrich the cDNA fragments upregulated by ischemia. Each of the PCR steps is tested with a range of template DNA concentrations, and the concentration giving the best signal is chosen for the next steps. The DNA mixture containing tester and driver DNA for the subtractive hybridization step is washed twice
5 with 70% EtOH by spinning for 3 minutes.

The second round cDNA subtraction is performed by hybridizing the first round cDNA subtraction product ligated to N-Bgl-12-24 oligonucleotides to an excess of the same driver cDNA used for the first round subtraction. The third round cDNA subtraction is performed by hybridizing the second round cDNA subtraction product ligated to J-Bgl-
10 12/24 oligonucleotides to an excess of the same driver cDNA used for the first round of cDNA subtraction at a ratio of 1:14,000. The final PCR product after the third round of subtraction is digested with DpnII to remove the oligonucleotides and ligated to pCR-Script SK(+) vector. This represents a selected cDNA library by RDA.

3(ii). Suppression subtractive hybridization (SSH) method to clone short-fragment cDNAs
15 up-regulated by ischemia

SSH is performed according to the manufacturer's instructions (Clontech, Catalog No. K1804-1) with certain modifications. Briefly, double-stranded cDNA are synthesized from mRNA isolated from rat kidney 24 hours or 48 hours post-ischemia as a tester, and from normal rat kidney as a driver with the Superscript Choice™ system for cDNA
20 synthesis (BRL Catalog No. 18090). The cDNA is synthesized according to the manufacturer's instruction except that the first strand cDNA is synthesized at 42°C. cDNA is digested with RsaI. Tester cDNA after RsaI digestion is ligated to adaptors. For the first hybridization, tester cDNA with adaptors is hybridized with excess driver cDNA at 68°C for 12 hours. For the second hybridization, the mixture is hybridized at 68°C for 22
25 hours. The cDNA mixture after the second hybridization is initially amplified by PCR for 27 cycles only. Then, a portion of the PCR product is re-amplified for 10 or 13 cycles. The final subtracted PCR product is digested by RsaI to remove the adaptor, and separated on a gel. The three bands and the remaining smear are cut out separately and cloned to pCR-

Script SK (+) vector (Stratagene, Catalog No. 211188). This represents a selected cDNA library by SSH.

4. Isolation and Characterization of Subtracted Amplified cDNA Clones

Colonies are randomly picked from the selected RDA and SSH cDNA libraries, and plasmid DNA is isolated with Qiagen plasmid kit. Each cDNA clone, referred to as a Subtracted Amplified Clone (SAC) is sequenced with the vector primers. DNA sequences are checked against GeneBank/EMBL databases for homology by the program BLAST™.

Southern blots are prepared with the initial PCR products generated from normal and injured rat kidneys. The blots are hybridized to the inserts isolated from the SACs to confirm which SACs are induced by ischemia.

4. Isolation and Characterization of potential full length cDNA clones

4.25 ug of polyA+ mRNA isolated from rat kidney 24 hours post-ischemia, which has been purified twice by oligo dT chromatography, is used to generate a cDNA library. In order to obtain double-stranded cDNA with EcoRI adaptors, a Superscript Choice® system for cDNA synthesis (BRL Catalog No. 18090) is used following the supplier's protocol, except that the cDNA synthesis reaction is carried out at 42°C. The DNA is ethanol precipitated, washed, resuspended in 5 ul H₂O, and ligated to 2 ug EcoRI digested and CIAP-treated Lambda ZAPII (Stratagene catalog No. 236612). The ligated DNA is packaged and used to infect E. coli XL-1 Blue MRF. The complexity of the library is 3.4x10⁶ independent recombinant plaques. Another cDNA library is generated from 4 ug of polyA+ RNA from rat kidney 48 hours post-ischemia as described above.

The two cDNA libraries described above are screened with inserts from the SAC clones. pBluescript plasmid vector containing cDNA inserts are excised from Lambda ZAPII vector by in vivo excision. Inserts from the longest cDNA clones, referred to as Potential Full Length (PFL) clones, are sequenced. DNA sequences are checked by the program BLAST™ against the GenBank/EMBL databases for DNA homology. Predicted protein coding regions (open reading frames, or ORFs) from some of the PFL clones also were used to search the GenBank/EMBL databases.

Diagnostic Uses of the Compounds of the Invention

Anti-KIM antibodies of the invention, which specifically bind to a protein of the invention or a unique fragment thereof, are useful in several diagnostic methods. These agents can be labeled with detectable markers, such as fluoroscopically or radiographically opaque substances, and administered to an individual to allow imaging of tissues which express KIM protein. The agents can also be bound to (conjugated to) substances, such as horseradish peroxidase, which can be used as immunocytochemical stains to allow visualization of areas of KIM protein-positive cells on histological sections. A specific antibody could be used alone in this manner, and sites where it is bound can be visualized in a sandwich assay using an anti-immunoglobulin antibody which is itself bound to a detectable marker.

Specific antibodies to KIM protein are also useful in immunoassays to measure KIM presence or concentration in samples of body tissues and fluids. Such concentrations may be correlated with different disease states. As an embodiment of particular interest, the invention includes a method of diagnosing renal injury, or of monitoring a process of renal repair, by measuring the concentration of KIM or of KIM fragments in the urine, plasma or serum of a patient. Similarly, KIM can be measured in urine sediment, in particular in cellular debris in the urine sediment. Casts of renal tubule cells, which may be present in urine sediment from patients with ongoing renal disease, may contain elevated levels of KIM protein and mRNA.

Specific antibodies to KIM protein may also be bound to solid supports, such as beads or dishes, and used to remove the ligand from a solution, either for measurement, or for purification and characterization of the protein or its attributes (such as post-translational modifications). Such characterization of an individual's KIM protein is expected to be useful in identifying deleterious mutants or processing defects which interfere with KIM function and are associated with abnormal phenotypes. Each of these techniques is routine to those of skill in the immunological arts.

Additional imaging methods utilize KIM or KIM fragments, fused to imageable moieties, for diagnostic imaging of tissues that express KIM ligands, particularly tumors.

Further diagnostic techniques are based on demonstration of upregulated KIM mRNA in tissues, as an indication of injury-related processes. (See, e.g., PCT publication no. WO 97/44460).

Therapeutic Uses of the Compounds of the Invention

5 The therapeutic methods of the invention involve selectively promoting or inhibiting cellular responses that are dependent on the presence or concentration of any KIM, including without limitation KIM ligation, KIM enzyme activity, KIM secretion, KIM signalling, and KIM modulation of gene expression. In instances where a KIM and a KIM ligand are both membrane bound, and expressed by different cells, the signal
10 transduction may occur in the KIM-expressing cell, in the KIM ligand-expressing cell, or in both.

 KIM ligation-triggered response in a KIM ligand-expressing cell may be generated by contacting the cell with exogenous KIM, KIM fusion proteins or activating antibodies against KIM ligand, either in vitro or in vivo. Further, responses of the KIM ligand-
15 expressing cell that would otherwise be triggered by endogenous KIM could be blocked by contacting the KIM ligand-expressing cell with a KIM ligand antagonist (e.g., an antagonist antibody that binds to KIM ligand), or by contacting the endogenous KIM with an anti-KIM antibody or other KIM-binding molecule which prevents the effective ligation of KIM with a KIM ligand.

20 Similarly, the responses triggered by KIM ligation in the KIM-expressing cell may be promoted or inhibited with exogenous compounds. For example, KIM ligation-triggered response in a KIM-expressing cell may be generated by contacting the cell with a soluble KIM ligand, or certain anti-KIM activating antibodies. Further, responses of the KIM-expressing cell that would otherwise be triggered by interaction with endogenous
25 KIM ligand could be blocked by contacting the KIM-expressing cell with an antagonist to KIM (e.g., a blocking antibody that binds to KIM in a manner that prevents effective, signal-generating KIM ligation), or by contacting the endogenous KIM ligand with an anti-

KIM ligand antibody or other KIM ligand-binding molecule which prevents the effective ligation of KIM with the KIM ligand.

Which of the interventions described above are useful for particular therapeutic uses depend on the relevant etiologic mechanism of either the pathologic process to be inhibited, or of the medically desirable process to be promoted, as is apparent to those of skill in the medical arts. For example, where KIM ligation results in desirable cellular growth, maintenance of differentiated phenotype, resistance to apoptosis induced by various insults, or other medically advantageous responses, one of the above-described interventions that promote ligation-triggered response may be employed. In the alternative, one of the inhibitory interventions may be useful where KIM ligation invokes undesirable consequences, such as neoplastic growth, deleterious loss of cellular function, susceptibility to apoptosis, or promotion of inflammation events.

Following are examples of the previously described therapeutic methods of the invention. One therapeutic use of the KIM-related compounds of the invention is for treating a subject with renal disease, promoting growth of new tissue in a subject, or promoting survival of damaged tissue in a subject, and includes the step of administering to the subject a therapeutically effective amount of a KIM protein of the invention, or of a pharmaceutical composition which includes a protein of the invention. The protein used in these methods can be a unique fragment of a full-length KIM protein, a soluble KIM variant or a soluble ligand thereof, a KIM fusion protein, or a KIM agonist. These methods can also be practiced by administering to the subject a therapeutically effective amount of an agonist antibody of the invention, or a pharmaceutical composition which includes an agonist antibody of the invention. A KIM protein can be administered concurrently with a therapeutically effective amount of a second compound which exerts a medically desirable adjunct effect. While tissues of interest for these methods include any tissue, preferred tissues include renal tissue, liver, neural tissue, heart, stomach, small intestine, spinal cord, or lung. Particular renal conditions which are expected to be beneficially treated with the compounds of the invention include acute renal failure, acute nephritis, chronic renal failure, nephrotic syndrome, renal tubule defects, kidney

transplants, toxic injury, hypoxic injury, and trauma. Renal tubule defects include those of either hereditary or acquired nature, such as polycystic renal disease, medullary cystic disease, and medullary sponge kidney. This list is not limited, and may include many other renal disorders (see, e.g., Harrison's Principles of Internal Medicine, 13th ed., 1994, which is herein incorporated by reference.) The subject of the methods may be human.

A therapeutic intervention for inhibiting growth of undesirable, KIM- or KIM-ligand-expressing tissue in a subject includes the step of administering to the subject a therapeutically effective amount of a KIM antagonist (e.g., an antibody blocks KIM ligation). In an embodiment of interest, the KIM antagonist or anti-KIM antibody can be used therapeutically to inhibit or block growth of tumors which depend on KIM protein for growth.

Other methods of the invention include killing KIM ligand-expressing tumor cells, or inhibiting their growth, by contacting the cells with a fusion protein of a KIM and a toxin or radionuclide, or an anti-KIM ligand antibody conjugated to a toxin or radionuclide. The cell can be within a subject, and the protein or the conjugated antibody is administered to the subject.

Also encompassed within the invention is a method for targeting a toxin or radionuclide to a cell expressing a KIM, comprising contacting the cell with a fusion protein comprising a KIM ligand and a toxin or radionuclide, or an anti-KIM antibody conjugated to a toxin or radionuclide. Another embodiment includes the method of suppressing growth of a tumor cell which expresses KIM, comprising contacting the cell with a fusion protein of KIM ligand and a toxin or radionuclide or with an anti-KIM antibody conjugated to a toxin or radionuclide; the cell may be within a subject, and the protein administered to the subject.

The term "subject" as used herein is taken to mean any mammal to which KIM can be administered. Subjects specifically intended for treatment with the method of the invention include humans, as well as nonhuman primates, sheep, horses, cattle, goats, pigs, dogs, cats, rabbits, guinea pigs, hamsters, gerbils, rats and mice.

Use of Compounds of the Invention in Gene Therapy

The KIM genes of the invention are introduced into damaged tissue, or into tissue where stimulated growth is desirable. Such gene therapy stimulates production of KIM protein by the transfected or transformed cells, promoting cell growth and/or survival of cells that express the KIM protein.

In a specific embodiment of a gene therapy method, a gene coding for a KIM protein is be introduced into a renal target tissue. The KIM protein is expected to be stably expressed and stimulate tissue growth, division, or differentiation, or to potentiate cell survival. Furthermore, a KIM gene can be introduced into a target cell using a variety of well-known methods that use either viral or non-viral based strategies.

Once introduced into a target cell, sequences of interest can be identified by conventional methods such as nucleic acid hybridization using probes comprising sequences that are homologous/complementary to the inserted gene sequences of the vector. In another approach, the sequence(s) may be identified by the presence or absence of a "marker" gene function (e.g, thymidine kinase activity, antibiotic resistance, and the like) caused by introduction of the expression vector into the target cell.

Formulation

In general, compounds of the invention are suspended, dissolved or dispersed in a pharmaceutically acceptable carrier or excipient. The resulting therapeutic composition does not adversely affect the subject's homeostasis, particularly electrolyte balance. Thus, an exemplary carrier comprises normal physiologic saline (0.15M NaCl, pH 7.0 to 7.4). Other acceptable carriers are well known in the art and are described, for example, in Remington's Pharmaceutical Sciences, Gennaro, ed., Mack Publishing Co., 1990. Acceptable carriers can include biocompatible, inert or bioabsorbable salts, buffering agents, oligo- or polysaccharides, polymers, viscosity-improving agents, preservatives, and the like. In some embodiments, the term "carrier" encompasses liposomes and the HIV-1 tat protein (See Chen et al., Anal. Biochem. 227: 168-175, 1995) as well as any plasmid and viral expression vectors.

Any KIM compound of this invention can be used in the form of a pharmaceutically acceptable salt. Suitable acids and bases which are capable of forming salts with the polypeptides, nucleic acids and vectors of the present invention are well known to those of skill in the art, and include inorganic and organic acids and bases.

5 KIM compounds of the invention are dispersed in the carrier to concentrations sufficient to deliver to the subject a therapeutically effective amount of the compound, which is an amount sufficient to produce a detectable, preferably medically beneficial effect in the subject. Medically beneficial effects would include preventing, delaying or attenuating deterioration of, or detectably improving, the subject's medical condition. It is
10 expected that the concentration or amount of a KIM compound that will produce a medically beneficial effect will vary considerably with the circumstances in which the invention is practiced. An effective amount can be determined by an ordinarily skilled physician or other practitioner through no more than routine experimentation. As an example, an indication of the status of renal injury or renal function can be monitored with
15 one or more routine laboratory tests which measure the concentrations of relevant substances in blood or urine, other urine characteristics, or the rate of clearance of various substances from the blood into the urine. The parameters measured by these tests, either individually or in combination, can be used by a physician to assess renal function or damage. Examples of such parameters include the blood concentration of urea, creatinine
20 or protein; the urine concentration of protein or of various blood cells such as erythrocytes or leucocytes; urine specific gravity; amount of urine; the clearance rates of inulin, creatinine, urea or ρ -aminohippuric acid; and the presence of hypertension or edema.

In some embodiments, a KIM compound is formulated in a liposome delivery system, including without limitation any of a variety of unilamellar vesicles, multilamellar
25 vesicles, or stable plurilamellar vesicles, all of which can be prepared and administered according to methods well known to those of skill in the art, for example in accordance with the teachings of United States Patent 5,169,637, 4,762,915, 5,000,958 or 5,185,154. In addition, it may be desirable to express the novel polypeptides of this invention, as well as other selected polypeptides, as lipoproteins, in order to enhance their binding to

liposomes. As an example, treatment of human acute renal failure with liposome-encapsulated KIM protein may be performed in vivo by introducing a KIM protein into cells in need of such treatment using liposomes. The liposomes can be delivered via catheter to the renal artery. The recombinant KIM protein is purified, for example, from
5 CHO cells by immunoaffinity chromatography or any other convenient method, then mixed with liposomes and incorporated into them at high efficiency. The encapsulated protein may be tested in vitro for any effect on stimulating cell growth.

Routes of Administration

The compounds of the invention may be administered in any manner which is
10 medically acceptable. Depending on the specific circumstances, local or systemic administration may be desirable. Preferably, the compound is administered via a parenteral route such as by an intravascular, intravenous, intraarterial, subcutaneous, intramuscular, intratumor, intraorbital, intraventricular, intraperitoneal, subcapsular, intracranial, intraspinal, or intranasal injection, infusion or inhalation. The compound also may be
15 administered by implantation of an infusion pump, or a biocompatible or bioerodable sustained release implant, or by installation of a catheter (e.g., in a renal artery), into the subject. Alternatively, certain compounds of the invention, or formulations thereof, may be appropriate for oral or enteral administration. Still other compounds of the invention will be suitable for topical administration.

20 Treatment Regimes

Determining appropriate dosage and frequency of treatment with any particular KIM compound to be administered to an individual is within the skills and clinical judgement of ordinary practitioners. The general dosage and treatment schedule is established by preclinical and clinical trials, which involve extensive but routine studies to
25 determine the optimal administration parameters of the compound. Even after such recommendations are made, the practitioner will often vary these dosages for different individuals based on a variety of considerations, such as the individual's age, medical status, weight, sex, and concurrent treatment with other pharmaceuticals. Determining the

optimal dosage and administration regime for each KIM compound is a routine matter for those of skill in the pharmaceutical and medical arts.

Equivalents

5 The invention may be embodied in other specific forms without departing from the spirit or essential characteristics thereof. The foregoing embodiments are therefore to be considered in all respects illustrative of, rather than limiting on, the invention disclosed herein. Scope of the invention thus is indicated by the appended claims rather than by the foregoing description, and all changes which come within the meaning and range of equivalency of the claims are intended to be embraced therein.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Sanicola-Nadel, Michele
Hession, Catherine A
Wei, Henry
Cate, Richard L
- (ii) TITLE OF INVENTION: MODULATORS OF TISSUE REGENERATION
- (iii) NUMBER OF SEQUENCES: 112
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Patent Administrator, Biogen, Inc.
 - (B) STREET: 14 Cambridge Center
 - (C) CITY: Cambridge
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02142
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/047,490
 - (B) FILING DATE: 23-MAY-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/047,491
 - (B) FILING DATE: 23-MAY-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Fenton, Gillian M
 - (B) REGISTRATION NUMBER: 36,508
 - (C) REFERENCE/DOCKET NUMBER: A028PCT
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 679-2810
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2058 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
(B) CLONE: HW010

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 8..646

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: complement (1618..1885)
(D) OTHER INFORMATION: /label= SAC_23807

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCGACA	GCT	CGG	ATC	CCC	CCA	TCA	CCT	ACC	TCA	CAG	ACT	GCT	CAG	ACA	49
	Ala	Arg	Ile	Pro	Pro	Ser	Pro	Thr	Ser	Gln	Thr	Ala	Gln	Thr	
	1				5					10					
GAA	GGT	AGT	AGG	ATC	ACA	TCC	AAA	ATG	CCT	GTG	GCG	TCT	ACC	CAG	GGG
Glu	Gly	Ser	Arg	Ile	Thr	Ser	Lys	Met	Pro	Val	Ala	Ser	Thr	Gln	Gly
15				20					25					30	
TCC	TCT	CCC	CCT	ACC	CCG	GCT	CTG	TGG	GCA	ACC	TCC	CCC	AGG	GCT	GCC
Ser	Ser	Pro	Pro	Thr	Pro	Ala	Leu	Trp	Ala	Thr	Ser	Pro	Arg	Ala	Ala
				35				40						45	
ACC	CTA	CCT	CCC	AAG	TCC	TCC	TCC	ACC	GGC	ACA	TCC	TGT	GAA	CCA	AAA
Thr	Leu	Pro	Pro	Lys	Ser	Ser	Ser	Thr	Gly	Thr	Ser	Cys	Glu	Pro	Lys
			50				55					60			
ATG	GTC	ATC	AAC	ACG	GTC	CCA	CAG	CTC	CAC	TCG	GAG	AAG	ACA	GTG	TAT
Met	Val	Ile	Asn	Thr	Val	Pro	Gln	Leu	His	Ser	Glu	Lys	Thr	Val	Tyr
	65					70						75			
CTC	AAG	TCC	AGT	GAC	AAC	CGC	CTG	CTC	ATG	TCT	CTC	CTC	CTC	TTC	CTC
Leu	Lys	Ser	Ser	Asp	Asn	Arg	Leu	Leu	Met	Ser	Leu	Leu	Leu	Phe	Leu
	80					85					90				
TTT	GTC	CTC	TTC	CTC	TGC	CTC	TTT	TCC	TAC	AAC	TGC	TAC	AAG	GGC	TAC
Phe	Val	Leu	Phe	Leu	Cys	Leu	Phe	Ser	Tyr	Asn	Cys	Tyr	Lys	Gly	Tyr
95				100					105					110	
CTG	CCC	GGA	CAG	TGC	TTA	AAG	TTC	CGC	TCA	GCC	CTG	CTG	CTC	GCA	AAG
Leu	Pro	Gly	Gln	Cys	Leu	Lys	Phe	Arg	Ser	Ala	Leu	Leu	Leu	Ala	Lys
				115				120						125	
AAA	AAA	CCT	AAG	TCA	GAG	TTC	TCT	GAC	CTG	GAG	CAG	AGT	GTG	AAG	GAG
Lys	Lys	Pro	Lys	Ser	Glu	Phe	Ser	Asp	Leu	Glu	Gln	Ser	Val	Lys	Glu
		130						135					140		
ACG	CTG	GTA	GAA	CCT	GGG	AGC	TTC	TCG	CAG	CAG	AAC	GGC	GAC	CAG	CCC
Thr	Leu	Val	Glu	Pro	Gly	Ser	Phe	Ser	Gln	Gln	Asn	Gly	Asp	Gln	Pro
		145					150					155			
AAG	CCA	GCC	TTG	GAT	ACC	GGC	TAT	GAA	ACC	GAG	CAG	GAC	ACT	ATC	ACC
Lys	Pro	Ala	Leu	Asp	Thr	Gly	Tyr	Glu	Thr	Glu	Gln	Asp	Thr	Ile	Thr
	160					165					170				
AGC	AAG	GTC	CCC	ACC	GAT	CGA	GAG	GAC	TCG	CAA	CGT	ATC	GAC	GAG	CTC
Ser	Lys	Val	Pro	Thr	Asp	Arg	Glu	Asp	Ser	Gln	Arg	Ile	Asp	Glu	Leu
175					180					185					190

TCC GCC AGG GAC AAA CCG TTT GAT GTC AAG TGT GAA CTC AAG TTT GCA	625
Ser Ala Arg Asp Lys Pro Phe Asp Val Lys Cys Glu Leu Lys Phe Ala	
195 200 205	
GAC TCG GAT GCC GAC GGG GAC TGAGGCCAGT GTGTCCCAGC CCGTGCCCCCT	676
Asp Ser Asp Ala Asp Gly Asp	
210	
CCGTC TTCGT GGAGAGTGTT GTGTTGAACC TATTCAGTAG CCGAGTCTTG TCACTGTGCA	736
CCAGCCTCAG TCTTTTGTCCT CTTTCTCTCT TGGGTGAGC CTGTGACTTG TCCCCCTTGT	796
CCTTTTGGA ACAAGTATC TATCAAGCC TCAAGTCCCG GCAGTTGTTG GAGCGCTTAC	856
TACACACCTG AGCCCTTGT GTCTGGGGG AGAGATGGCC ACCTCCGTGG GCTGAGAAGA	916
ACCACCCCTT CTTCTCCGC TCCTCGAAGC AGCCACTGAG AGATAATTTA ATTCCAGATT	976
GGAAATGACC TTTTGGTTT ATCAGATTGG TAACTTAATC TCCTGCCATC CGGGTGGCAC	1036
GGACGT TTTT CTTTCACTTC GTTATTTTTT TTAGGATTTG CGCTCCTACT GTGTTGATGT	1096
CTTAGGTCAT TTTTTTTTTT TTAAGTTACC AGAGGAGATG TTTTGATATT CATGAGAAGA	1156
AGAACATTTT CTAGATTTTT TTTTTTTTTG GTTACATATT GAGATAAAAT ATGCCTCTGT	1216
TGCTTAAGAT TCTCAGGGAT AGACGTGATT TTTGCTAATT TCTTTCCTGC TGTTCGGAAC	1276
GTAGGCCTAA AACTGTCTCT TGAGCTCACA CACTCACCTT TCCTTTTGG TGGGTTTTTT	1336
TTTTTTTTTG TTTTGT TTAATCTTAC TCATTTTCGAA GGATTTTCTT TATGAGCTTT	1396
TGTTTTGTTT TTGTTTTGTT TTTTGT TCTCTTTTTC CTGCCGTACA TCATCTACGA	1456
GGTGCGTTTT GAGTGAGGGC AGATGGCCCA GTGGCTTCGG GTGGCCAGT GGCTGTGGGT	1516
GGCAGTTGAG CTGGTCCTGT GAGGGGAGGA GGGCTTAGAC GCCACGGCCC TGCTGCTTCT	1576
CGGCACCTCC TGTCCTGATG GGTGGCGTCT TCATGAGGAT TACATCCTGT CTCTGCTGGC	1636
TTCCATCTCG CACCTCTGCC CTTGGACTTC CACCTTGACT GTCCACAAA GACAGAAATG	1696
GGCTGGCTAG TTGGGCTCCC GGCCTCGGAC GGTGGCCGCA ACGTCCCGTG TGGGCGGCTG	1756
CCGTCGCAGC CTGACTCCTG CCGGTGTCTT TCAGGATGTG AACGGGTGGT ACGAATCTTG	1816
ACATTTGTTT CTCACTTCCT GTGTATGAAA CGACACTCAT TCCATGTAGA GGGTGACGGA	1876
CTCTGGATCC CCCCCCTTGT CGTGTAGACA CTCATCTTCA GCGTGACCTG GTCCTGCCAT	1936
TCGGTGTAAC CATTTGTGTT TATAAGATTT ACTTTGTTTT TATTTTCTA CTTGGAAC TG	1996
TACATATTTG AAAAAGTACC CAAATAAACC AGAAGCTTTA TCGTTGAAAA AAAAAAGTCG	2056
AC	2058

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Ala Arg Ile Pro Pro Ser Pro Thr Ser Gln Thr Ala Gln Thr Glu Gly
 1           5           10           15
Ser Arg Ile Thr Ser Lys Met Pro Val Ala Ser Thr Gln Gly Ser Ser
          20           25           30
Pro Pro Thr Pro Ala Leu Trp Ala Thr Ser Pro Arg Ala Ala Thr Leu
          35           40           45
Pro Pro Lys Ser Ser Ser Thr Gly Thr Ser Cys Glu Pro Lys Met Val
          50           55           60
Ile Asn Thr Val Pro Gln Leu His Ser Glu Lys Thr Val Tyr Leu Lys
 65           70           75           80
Ser Ser Asp Asn Arg Leu Leu Met Ser Leu Leu Leu Phe Leu Phe Val
          85           90           95
Leu Phe Leu Cys Leu Phe Ser Tyr Asn Cys Tyr Lys Gly Tyr Leu Pro
          100          105          110
Gly Gln Cys Leu Lys Phe Arg Ser Ala Leu Leu Leu Ala Lys Lys Lys
          115          120          125
Pro Lys Ser Glu Phe Ser Asp Leu Glu Gln Ser Val Lys Glu Thr Leu
          130          135          140
Val Glu Pro Gly Ser Phe Ser Gln Gln Asn Gly Asp Gln Pro Lys Pro
          145          150          155          160
Ala Leu Asp Thr Gly Tyr Glu Thr Glu Gln Asp Thr Ile Thr Ser Lys
          165          170          175
Val Pro Thr Asp Arg Glu Asp Ser Gln Arg Ile Asp Glu Leu Ser Ala
          180          185          190
Arg Asp Lys Pro Phe Asp Val Lys Cys Glu Leu Lys Phe Ala Asp Ser
          195          200          205
Asp Ala Asp Gly Asp
          210

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1727 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW011

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCGACATGA TTGCTAGTGG TTCTGCTGGC TGTGAGGGCT CCCTGTCTGT GAGATCTTGT	60
TCGGGCTTTC CACATCCAGG ATCCATCCAT TCACCCCTCA CCCACTCACC CTGTGGAGCA	120
TAAAACCTTT GCAGTCAGCC AGCATGGCAG AATGTCATATG CCTTGCTTCA GTTCCAGGG	180
TAACCTAAGCA TGTTTTTAATC CCACTGCCCC ACCCACTATT GCTCATTTCTG TCTAGTCTTC	240
TGCTACCCAG CTGTGTGGC TCCGTTCTTG TCACGCCTTC AGACGTCACCT GTTCTGTGAC	300
AGCGGTCTCT TTCCCCTCTG CTCCACCCAT TCTGAGCTCT GGGATAGTCC TAAGCCCTGC	360
CCAGAGTAGG TGGACTGGTC GTTCCATGTC CGTGCTTTGTG GGAGTTGTGG GGGTCTGTGG	420
CATCTGCTAA GGAGGTTTAT CCTCACGTCA CGGAATCCGG CAAGATGCGC CATGGTCTAC	480
ACTGCTTTCT CGAGCAGCGG CGAGAAAGGC CAGGATAACA CACGCCCTCTC TGCCCTGAGA	540
TAACAACTG TCTGAGAAAG GAAGTGGCCC GTGTCTGGAA CATTGGCCCC AGTAAAGCAG	600
AGGAGACACT GCCATGTTTC CGTCATTTCTG TTCACTGCC TTGCTCTGGG GCTCAGGGGT	660
TGAAGAATGA GGATACACCA TTCGACCTTC AGGCCTTCCT CAGACCCTCT TACAAAGCCT	720
GTTGTTGTGA GTCCAGCTCA TCAGCATGGC CGCCTTGTTT ACAGTTTAGC ACCAGTGTCT	780
GCAACCGTGT CTGAAACGTA GCAGATGTCC AGTACTTTTT GTAAATGAAA AAATGAACAG	840
AGTGAAGAGA AAGAGTCACC ATGAAATTTA CTAGTCCAGT GAGCTGACCG TAGGGGCAGT	900
ATAACATCC CCCAGCTCTT AATGTTCTGT CCTCAAGCTG TCCCCTCCCA CCTCTCCGCT	960
GGCAGGAGAG TGCTCTGTAT ATGTGGACAG TCGTTGAATG GCAGGTCCAG GATGTCCTCT	1020
GCAGGTGGAC AAAAGAGAAT TCTGCTTCCC GGAAGTCTCC TTTGCTGGTG ATCTCCATGT	1080
CCATCTCAC TGAGCACTAG AATTAAAACC ACTCAATAAT GTGATATGTG TGGTCACCTT	1140
CAGTTCAGTA GCAGTATTTT CTGGTCATTA ATATTTCTGCA TTTTATTATG GTAAGATAGT	1200
ATAAGAAAAT GGTGGGCTGG TATATAGCCA GCCATGAGAC CACTCCTTAC GTCAAGGACT	1260
GGCAGAGTCT GAGGGACCTG AGTCTGGGTC CTCTCCTGT CCCCTCCTCC TGTAGCTATG	1320
GTGGCCTTCA GTATTCTGAG ACTGAAGGCT ACTACTTCAG GACACCTACT TGATCTTAGT	1380
ACTCTCAGAA CAGCTCTCCT CAGTTCTAGC TGTGATCGCG GGCTGCGTTT GGAACGTTAA	1440
CGTACTAATG GGTTTAAGAC TTTCAGAAAG TGATTTTAAA ACAAATGAC TGGAAGTTTT	1500
GTCTGATAAA GCAAGTAGAA TGGAATGTCT CAGACTGTCT CGTCACATTT TCATGTTTCA	1560
TACGAAAAGA AAAGATTGAT AACCTATCTT TAGAAATAGT AATGTTAGTT CTTTCCTATT	1620
TTGTTTAAAC CTTGAAGAAG GTTTTATTTA ACTCGTGAAC TTGTTCTTTT GTTATGACAT	1680
GATTGTTCCA GATTGAGGG ACAAATAAAA ATTAACCTTT CTAAAAA	1727

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1060 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW012

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 39..671

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTCTGACGCAT GGGTGCAGGT GACAAATGAG CTGAAGAA ATG ATC CCC AGA GGA	53
Met Ile Pro Arg Gly	
1 5	
ATA GGA TTG TGG CTG CCT TCA GCT CTG CTC CTC TCT CGG GTC CCA GGC	101
Ile Gly Leu Trp Leu Pro Ser Ala Leu Leu Leu Ser Arg Val Pro Gly	
10 15 20	
TGT TTC CCT CTG CGT GGC CCC AGC AGT GTG ACA GGC ACT GTG GGG GAG	149
Cys Phe Pro Leu Arg Gly Pro Ser Ser Val Thr Gly Thr Val Gly Glu	
25 30 35	
TCC CTG AGC GTG ACT TGT CAG TAT GAG GAG AGA TTC AAG ATG AAT AAG	197
Ser Leu Ser Val Thr Cys Gln Tyr Glu Glu Arg Phe Lys Met Asn Lys	
40 45 50	
AAA TAC TGG TGC AGA GGG TCA CAT GTT CTA CTT TGC AAA GAT ATT GTC	245
Lys Tyr Trp Cys Arg Gly Ser His Val Leu Leu Cys Lys Asp Ile Val	
55 60 65	
AAG ACC GGA GGC TCA GAA GAA GCT AGA AAT GGC CGA GTG TCC ATC AGG	293
Lys Thr Gly Gly Ser Glu Glu Ala Arg Asn Gly Arg Val Ser Ile Arg	
70 75 80 85	
GAT GAT CCA GAC AAC CTG ACC TTC ACA GTG ACC TTG GAG AGC CTC ATC	341
Asp Asp Pro Asp Asn Leu Thr Phe Thr Val Thr Leu Glu Ser Leu Ile	
90 95 100	
CTG GAG GAT GCA GGC ACC TAC ATG TGT GGG GTG GAT ATA CCA TTT ACT	389
Leu Glu Asp Ala Gly Thr Tyr Met Cys Gly Val Asp Ile Pro Phe Thr	
105 110 115	
AAT CAC CCC TTG GGG ATT GAT GAG TTC TTC AAG GTT GAA TTG TCT GTG	437
Asn His Pro Leu Gly Ile Asp Glu Phe Phe Lys Val Glu Leu Ser Val	
120 125 130	
GTC CCA GGT TCA AGC CTT TGG AGC AGT ACA ACA GTC CCA GAG ACC ATC	485
Val Pro Gly Ser Ser Leu Trp Ser Ser Thr Thr Val Pro Glu Thr Ile	
135 140 145	

AGA TCC TCA CTG GTT CAT ACT CAG CCC AGT GTG ACC ACA GAA GAC ACA 533
 Arg Ser Ser Leu Val His Thr Gln Pro Ser Val Thr Thr Glu Asp Thr
 150 155 160 165

ATT CCT GCT CCT AGT GCA CGG CCT CGG TCT CTT CTG GGC AGC CTC TAC 581
 Ile Pro Ala Pro Ser Ala Arg Pro Arg Ser Leu Leu Gly Ser Leu Tyr
 170 175 180

CTC TGC ATC CTG GTG TTT CTG GAG TTG CCC CTG TTC CTG TGC ATG CTC 629
 Leu Cys Ile Leu Val Phe Leu Glu Leu Pro Leu Phe Leu Cys Met Leu
 185 190 195

TGT GCC GTC CTG TGG GTG AAC AGG CCT CAG AGG TGC AGT GGG 671
 Cys Ala Val Leu Trp Val Asn Arg Pro Gln Arg Cys Ser Gly
 200 205 210

TGACATAGCA TTGGGCCCTG TCATGAGTAC CAGTGAAGTC TGTTGATATG GAGGCCCTGT 731

CCCTGGATGC ATCACCTCTG GTGGCCAAGG ACAACCAATA AAGCTGTGTT CTTGAGAATG 791

CTCTGAGACT TTTAGAAGAT TCTCTGCACG TGTCAAACAC ATAAAAGAAT GTGCCCAATA 851

AATACCAGCT GGGGAATTGG CTCAGCAGGT AACAACAATG GCTGCTTTTC CAGAGGTCCT 911

GAGTTCAATT CCAATAACTA CATCGGTGGC TCACAACCAT CTCTAATGAG TTCAGATGCC 971

CTCTTCTGCT GTGCAGGTGC ACATTACAT AGAATATTCA TACATTGAGT AAATTTATTA 1031

AAAGTAATTG CAGAATTAAA ACACAAAAA 1060

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ile Pro Arg Gly Ile Gly Leu Trp Leu Pro Ser Ala Leu Leu Leu
 1 5 10 15

Ser Arg Val Pro Gly Cys Phe Pro Leu Arg Gly Pro Ser Ser Val Thr
 20 25 30

Gly Thr Val Gly Glu Ser Leu Ser Val Thr Cys Gln Tyr Glu Glu Arg
 35 40 45

Phe Lys Met Asn Lys Lys Tyr Trp Cys Arg Gly Ser His Val Leu Leu
 50 55 60

Cys Lys Asp Ile Val Lys Thr Gly Gly Ser Glu Glu Ala Arg Asn Gly
 65 70 75 80

Arg Val Ser Ile Arg Asp Asp Pro Asp Asn Leu Thr Phe Thr Val Thr
 85 90 95

Leu Glu Ser Leu Ile Leu Glu Asp Ala Gly Thr Tyr Met Cys Gly Val
 100 105 110

Asp Ile Pro Phe Thr Asn His Pro Leu Gly Ile Asp Glu Phe Phe Lys
 115 120 125
 Val Glu Leu Ser Val Val Pro Gly Ser Ser Leu Trp Ser Ser Thr Thr
 130 135 140
 Val Pro Glu Thr Ile Arg Ser Ser Leu Val His Thr Gln Pro Ser Val
 145 150 155 160
 Thr Thr Glu Asp Thr Ile Pro Ala Pro Ser Ala Arg Pro Arg Ser Leu
 165 170 175
 Leu Gly Ser Leu Tyr Leu Cys Ile Leu Val Phe Leu Glu Leu Pro Leu
 180 185 190
 Phe Leu Cys Met Leu Cys Ala Val Leu Trp Val Asn Arg Pro Gln Arg
 195 200 205
 Cys Ser Gly
 210

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3385 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW013

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTCGACTTTT TTAAACAAAG ATGATTTAAT ATTTAATATC ATACCCAGAA AAATCAAACA	60
ACTTCCAGAA TCAGACAGGT AAGATTCCCTT AGTATGTTTT TACCAAAATT TTATAAGATT	120
ATCTTAAATT TGAAGAATTG TGCATAAATA ACACAGGATA CCAAAGGAAA CTGAGCTGTA	180
TTTTTTGCTT TGATGGGAAA AAAAAAAAAA AAAACCTGAA ACCCAGAGAC ACTAACCATT	240
TTGTGCACTG TATAACTCAT TGTGGAAGCT GAAACTTAGA ACTCATCTTT GGAAATATAT	300
AATTGATGAA CCCACCTTTC CATTCAGCTT TTAGGGTGAT GTAAACTGT ATGAATCCAC	360
TTACAAATAA ACTTAAAAGA CCTTTTCATG TTACCCTATC TCTTATCTTC TCAATGTATT	420
TCTATATGCT TACCTTTAGT AAGAGTACCA TGGAGTACTT TGATAGATGG AATGACAGAG	480
AAATGGATGT TTAAAGATCT TTAGGATGAA AAGGATAATT TAAGAAGCAT ATTTAAGAAG	540
CATGCTGATA TTGAAAAGGT AGTATAGGCA AGTACAGTGC ACTTCCACAG ACTACTCATA	600
CCTTCTTGTC CATCAGAAAG TCTGAGTGGG TTAGTTACAG TAAGGTCATG TTGATCTGGG	660

TCTATGCACC	TGTGCTGAGG	TCAGAGGACA	ACTTTCAGGA	GTCTGTTCTG	CCCTTCCGTG	720
TGGGTCCTAA	GTATGCAACT	CAAAGGTTGT	CTGTCAGGTT	GATTCTGCCC	AGTCATGAAA	780
CCTTTGAGAA	GAGGAAAAGG	TGTAGGAAGA	ACAGGAACAG	GATCATAGAA	GTGACTAAGC	840
CAGAATCTGT	CATATTTGAG	GAAACATCAA	GAGGTGCCTA	TAATAGGGTT	CCGAGAATGA	900
AAAAAAAAAC	CAGATAACTT	TACTGTCTAT	TCCAGCCAGT	TTGACTTAGA	GGCACTGGCA	960
AAGTAGGTAC	AGACAGCTGA	GGTAGAAAAT	GTGGAAACATT	ACTGTGGCAA	CTGCTGCATC	1020
TTCGGGTGTG	GAAGTCACAC	CAATTCCTACT	TTTGGTTGGC	ACTTCCCATC	TTCTAAGAGA	1080
GAACCTTTAA	TTGAGCGGCC	GTGAAGAACT	TGATAAATCT	ACGCTGCTGT	GTGTCTCTCA	1140
CCACCACCCT	ACCTACATAG	ACACCCCAT	TTAGTTGTTT	CCTGAGAATC	AGAACAGAGC	1200
ACTTACACGA	GGTACGGGAA	GCTGTGATGC	CTAGTGTAAG	AAGTTAGAAG	ATGACTGAAC	1260
ACAGGAAGAG	AGCGGGCTTC	CAGTGGGATC	TAAATCAAAT	CAGCGAGGAT	CACTGGAAAC	1320
TGAGCTGAAA	CTCAACTAAG	ATTTAGCTTG	CAAACAATAG	AGATGTTTCA	TTTTAAAACC	1380
ACAGCAGATT	AACAGTATAG	CTGGGAAACA	ACCAAGTGTT	CTTTTCAAAT	TTCAAGTTCCA	1440
CTATATCTGA	GATGGTTAA	AATAGGGGTG	AGTCCTATTT	CATGGCTTTT	ATCTATTAAA	1500
TATTTGTAAA	CGTGCTCAAG	TTCCCATTTT	TTTAAACCCTA	CAAAATTCAG	GCTTCTCACA	1560
CTGGGGCTGT	AGTTCCTTAA	TAGTTTTCTA	ATTCTGAGC	CATCTTTAGA	CTTCTGAAAA	1620
CCTCAACTTC	AGTCTCTTCT	CACATAGCCA	ACTATGAGAA	CCTCCAAAGC	AGAATGCAGT	1680
TTTCCTTGTTG	CCTTTAGCAA	CAAGGCACCT	TTACAAAACCT	GGTTCTCAGT	GAATGAAATG	1740
AAAGCATGAT	CTTACAGTGT	GCGACACTTC	AGTAGTGATG	ACTTAGAATA	GTTTTAAAAT	1800
AAATAAAATT	ACAGAACCTA	GGGGAGGTGA	AAAATGGGAA	ACATGAAACA	GTAGACCATA	1860
CTGCAGCTCA	CAAAACAAGC	AGTGAAAACA	TATAAACTAC	CTATAATAGC	CTCATTATAA	1920
CATGCAAAACA	CACCTAACTCT	GTTACATACA	GATTGGATGT	ATATCTGAAG	TGTGTTATAG	1980
ATACAATGGG	TTTAAGTTGG	TAATTAATAA	ATAGTACTAC	CTTAGAATGT	GTTGTGCTTT	2040
TAAGTATTAT	GAAAGCTCAA	GAGCCAGGCA	TCTTCCTCTT	CAGAGCTGTT	TCCTGTTACA	2100
TAAITACTGG	CAAAGTTCTA	AACAGTTCTT	TACTAAATCA	CAAAATGCAT	ACAGCTAGTG	2160
CCATTGTCTC	AAGTCTTTTT	AGAATAGAAA	TGTCGATGTG	AAGCTATAAT	TTTATTTTGG	2220
TTTTATGATC	CTGCAAGGGT	TAAGTTTGTC	TGATTCTTCC	CAGGGTACTG	ATAAGTTCTC	2280
TAACATACCG	GAGTAAGAGA	ACTGAAACAG	GTTATTTCCC	TCATCCTCAG	GAATCTGCTT	2340
GAATATGGAT	CAGCATATAT	TGGACTTAAT	GCTGCTTTTG	GGGGCCTAAT	AGCAAACAGT	2400
CTATTTCCGC	GAATTTTGAA	CGTGACACAA	GCTCGAGTAG	CATCTAGCTT	GCCAATGGCT	2460
GTGATCCCAT	TTTTGACAGC	AAACCTGTCC	TACCATAGTT	TGTAAAGTTT	ACCTTTGAGT	2520
ACAGGTATGT	TTTATTTTCAT	TATCATCCAA	GCCTGCATTT	ATGCATACTA	TATACACTTA	2580

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TATATACTTC ACTCAAACT GAAGGATTAG AACCGAGTAG GTGTGAGCTT TAATGAAGTG      2640
TTTAGGGAAG ACCAAATCTA TTCAACAACT GATTCAGCTT AGGTCTGCCA ACCAACCAGT      2700
GAGTACATAT CCACAGCCGT CAGTCACACA CTTCCCTGAC CTGAAGCAGC ATTCCCAGTG      2760
CTGCCTTTGT TTCTTGTTAA TTTGCACATT ATATGCAAGT TTTCTCTTTT TAAAAAGATG      2820
TTTTTATTTA GGTATGTGTT TTGTCTGACT GTACATTTGC ACACCAGGTA GTGGTACTGG      2880
ACCCCATATA CTAGTTACAG ATAAGGGTGA GCTGCCACGT GGGTGCTGGT AATTGAACTC      2940
AGCACTTAGT GCCATTGCTC TTAATTGAGA TCTCTCTCCA GCCCTGTATG AAAGTTCTTT      3000
AAAGTATAAG TATGTTGTGG GAATACAACT CTGTAATCTC TGAAGTACTA TGTGCATTGC      3060
AGCATTTAGC AAAATGAAAG ACATAGTGTC CCATGTGTCC TGAACATGTA TTGTTATGTG      3120
TTCTATATGC ATGACCCTTC TTATTAAAAA CAGATTGGGG AAAGGGGTCA ATTTTGTGTT      3180
TTCTCCTAAA TAATAATCCA AATTCTGAG AATCCAGAGT CAAGATTTGT TTTCCTGTTT      3240
ATCAGTATTT CCTATCCAAG GCCTTAATAC ATGCTAAGCA TGTATTCACA CCAAGCTACA      3300
GTCCATCCTC TATAATTATT CCTTTGACAT GATATGCACC ATTTTGTCTG TGTCAGTAA      3360
AATAAAATGT GAACCTTATG TCGAC                                          3385

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(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1779 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW014

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 175..804

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

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GTCGACCTGG AAAGAGCTGC AGTGTTCGCG CTTGGTAGCT GGTGGACCGG GCTCAGCACC      60
TTCGGCTGGC TTTGTGTCCC AGAGGCTCAC CGGAAAAAGA CTTTCTCAGC CCTCGGACTC      120
CAGAGAGAGA TACTTTTCGT GCTCCCAAC CTTGACTCCT GCAGAAGCTG AGCG ATG      177
                                         Met
                                         1
GCG TCC ATG GGG CTG CAG GTG CTG GGA ATC TCC TTG GCC GTC CTG GGC      225
Ala Ser Met Gly Leu Gln Val Leu Gly Ile Ser Leu Ala Val Leu Gly
      5              10              15

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TGG	TTA	GGA	GTC	ATC	CTG	AGT	TGT	TCG	CTC	CCC	ATG	TGG	CGG	GTG	ACC	273
Trp	Leu	Gly	Val	Ile	Leu	Ser	Cys	Ser	Leu	Pro	Met	Trp	Arg	Val	Thr	
	20						25					30				
GCC	TTC	ATC	GGC	AGC	AAC	ATC	GTC	ACG	GCG	CAG	ACG	AGC	TGG	GAA	GGC	321
Ala	Phe	Ile	Gly	Ser	Asn	Ile	Val	Thr	Ala	Gln	Thr	Ser	Trp	Glu	Gly	
	35					40				45						
CTG	TGG	ATG	AAC	TGC	GTG	GTG	CAG	AGC	ACC	GGC	CAG	ATG	CAG	TGC	AAG	369
Leu	Trp	Met	Asn	Cys	Val	Val	Gln	Ser	Thr	Gly	Gln	Met	Gln	Cys	Lys	
	50				55					60					65	
ATG	TAC	GAC	TCG	ATG	CTG	GCC	CTG	CCG	CAG	GAC	CTG	CAG	GCC	GCC	CGA	417
Met	Tyr	Asp	Ser	Met	Leu	Ala	Leu	Pro	Gln	Asp	Leu	Gln	Ala	Ala	Arg	
				70					75					80		
GCC	CTG	ATG	GTC	ATC	AGC	ATC	ATC	GTG	GGT	GCT	CTG	GGG	ATG	CTT	CTC	465
Ala	Leu	Met	Val	Ile	Ser	Ile	Ile	Val	Gly	Ala	Leu	Gly	Met	Leu	Leu	
			85					90					95			
TCA	GTC	GTA	GGG	GGC	AAG	TGC	ACC	AAC	TGC	ATG	GAG	GAC	GAG	ACC	GTC	513
Ser	Val	Val	Gly	Gly	Lys	Cys	Thr	Asn	Cys	Met	Glu	Asp	Glu	Thr	Val	
		100					105					110				
AAG	GCC	AAG	GTC	ATG	ATC	ACA	GCC	GGA	GCC	GTG	TTC	ATC	GTG	GCA	AGC	561
Lys	Ala	Lys	Val	Met	Ile	Thr	Ala	Gly	Ala	Val	Phe	Ile	Val	Ala	Ser	
	115					120					125					
ATG	CTG	ATT	ATG	GTG	CCT	GTG	TCC	TGG	ACG	GCA	CAC	AAC	GTC	ATC	CGC	609
Met	Leu	Ile	Met	Val	Pro	Val	Ser	Trp	Thr	Ala	His	Asn	Val	Ile	Arg	
	130				135					140					145	
GAC	TTC	TAC	AAC	CCT	CTG	GTG	GCT	TCC	GGG	CAG	AAA	AGG	GAG	ATG	GGG	657
Asp	Phe	Tyr	Asn	Pro	Leu	Val	Ala	Ser	Gly	Gln	Lys	Arg	Glu	Met	Gly	
			150						155					160		
GCC	TCG	CTT	TAC	ATC	GGC	TGG	GCG	GCT	TCT	GGG	CTG	CTG	CTC	CTG	GGA	705
Ala	Ser	Leu	Tyr	Ile	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	
			165				170						175			
GGA	GGC	CTC	CTC	TGC	TGC	AAT	TGC	CCA	CCT	CGC	CGC	AAC	GAA	AAG	CCC	753
Gly	Gly	Leu	Leu	Cys	Cys	Asn	Cys	Pro	Pro	Arg	Arg	Asn	Glu	Lys	Pro	
		180					185					190				
TAC	TCC	GCC	AAG	TAC	TCC	GCC	GCC	CGC	TCT	GTT	CCC	GCC	AGC	AAC	TAT	801
Tyr	Ser	Ala	Lys	Tyr	Ser	Ala	Ala	Arg	Ser	Val	Pro	Ala	Ser	Asn	Tyr	
	195					200					205					
GTG	TAAGGTGGGC	CACTCTCTGT	CCACATTGCC	TTTATTTTCT	TGGATTGAAC											854
Val																
	210															
TCATAACGGC	CTGTGGCCCC	TCACATTCTC	CAGGACCTGA	CCAGCTGTGG	GCTACTGACT											914
GCTTGCAAAC	CCGGACTGTG	CTAAGTTACT	AGCGTGTAGC	CCTTGGGGAC	CCACCTGGCC											974
CATCTGGACA	CATCTCAAGG	CTCCAGCGAG	GATAGATGTA	AAAATATTTTC	CTTGCTTGCA											1034
TCCAGATTGC	TCATGGATAC	GGGGCTGAAG	GCAGAAGCAG	CTGTCTGGGT	ACGACAGTGG											1094
AGGGGGAGCT	GGGTCCTGCT	GGCCGGGATA	GCTCAGCTGT	GACTTTGGTC	TCTGGAGTGG											1154

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ATGTCCTGGT CATGTTAGCA AACATTCACT GCCCTTTCTC AGTGCCCTCG CTCTCTCGCC      1214
TCCACGTTAC TCCCGCGCTA CTCTTGCCGT TTCTCGCCCG CGTTTCTGAG CACACCAGGT      1274
CCTGCCCTGA GTCTTGGTGT CGAGGATGAC TGACTGAAGG GGCCTTTGAG AGCTGATGGG      1334
TTCTGCCATG GACTCCTCCC GGTGATTAGC AATGACTGGG GCCTTACCCA CCCACCTACC      1394
CTCGTAATGA AGTCTGTGG AGTGCTGGA CAGGTTTGAG GGAAGGGTGG AGGTGGTTTA      1454
AACTGGTTTG GGGAGTGCTA GGGCTGGGGA CCCAGAAGCA GCCCAGGGTG TCCCCACCCC      1514
TTTCCCATAC GGTCTTGCTA AATGTTCTGA TCTCTGTATA CCCCCTCCCT CTTCAGAAGG      1574
ACCCTGGGTG GGCCCTCTG AATTCCTTAC CCTGTCCAT TTCAAGGACG CTGGCCAGTC      1634
TGTGGAAGGT ACGGGGTCT GATGGCATTG CACCAGGGAG CCTCCTGGAC TCCCTTGCCT      1694
TCTCTGTGGT TTCTGTGTTT GTAATTTAAG GTCTGTTTAC AGCTGTAATT ATTATTTTCT      1754
ACAATAAATG GCACCTGCAG TCGAC                                          1779

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Met Ala Ser Met Gly Leu Gln Val Leu Gly Ile Ser Leu Ala Val Leu
 1           5           10          15
Gly Trp Leu Gly Val Ile Leu Ser Cys Ser Leu Pro Met Trp Arg Val
 20          25          30
Thr Ala Phe Ile Gly Ser Asn Ile Val Thr Ala Gln Thr Ser Trp Glu
 35          40          45
Gly Leu Trp Met Asn Cys Val Val Gln Ser Thr Gly Gln Met Gln Cys
 50          55          60
Lys Met Tyr Asp Ser Met Leu Ala Leu Pro Gln Asp Leu Gln Ala Ala
 65          70          75          80
Arg Ala Leu Met Val Ile Ser Ile Ile Val Gly Ala Leu Gly Met Leu
 85          90          95
Leu Ser Val Val Gly Gly Lys Cys Thr Asn Cys Met Glu Asp Glu Thr
100         105         110
Val Lys Ala Lys Val Met Ile Thr Ala Gly Ala Val Phe Ile Val Ala
115         120         125
Ser Met Leu Ile Met Val Pro Val Ser Trp Thr Ala His Asn Val Ile
130         135         140
Arg Asp Phe Tyr Asn Pro Leu Val Ala Ser Gly Gln Lys Arg Glu Met
145         150         155         160

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Gly Ala Ser Leu Tyr Ile Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu
 165 170 175
 Gly Gly Gly Leu Leu Cys Cys Asn Cys Pro Pro Arg Arg Asn Glu Lys
 180 185 190
 Pro Tyr Ser Ala Lys Tyr Ser Ala Ala Arg Ser Val Pro Ala Ser Asn
 195 200 205
 Tyr Val
 210

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: HW015
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 11..2176
 - (D) OTHER INFORMATION: /product= "predicted polypeptide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCGACCAAA ATG GCA GCC TTG GAA GAA GAA TTC ACG TTG TCT ACT GGA	49
Met Ala Ala Leu Glu Glu Glu Phe Thr Leu Ser Thr Gly	
1 5 10	
GTC TTA GGC GCC GGG CCT GAA GGA TTC CTA GGT GTA GAG CCC AGT GAC	97
Val Leu Gly Ala Gly Pro Glu Gly Phe Leu Gly Val Glu Pro Ser Asp	
15 20 25	
AAG GCC GAC CAG TTC CTA GTG ACC GAC AGA GGC AGG ACC GTC GTC CTC	145
Lys Ala Asp Gln Phe Leu Val Thr Asp Arg Gly Arg Thr Val Val Leu	
30 35 40 45	
TAC AAG GTT TCT GAC CAG AAA CCC TTG GGC AGC TGG TCG GTG AAA CAA	193
Tyr Lys Val Ser Asp Gln Lys Pro Leu Gly Ser Trp Ser Val Lys Gln	
50 55 60	
GGC CAG ACT ATA ACA TGT CCT GCT GTG TGC AAC TTT CAG ACT GGA GAG	241
Gly Gln Thr Ile Thr Cys Pro Ala Val Cys Asn Phe Gln Thr Gly Glu	
65 70 75	
TAT ATT ATG GTA CAT GAC CAT AAG GTT TTG AGA ATA TGG AAT AAT GAA	289
Tyr Ile Met Val His Asp His Lys Val Leu Arg Ile Trp Asn Asn Glu	
80 85 90	
GAC GTA AAC CTG GAT AAA GTA TTC AAA GCT ACA CTG TCA GCT GAG GTC	337
Asp Val Asn Leu Asp Lys Val Phe Lys Ala Thr Leu Ser Ala Glu Val	

95	100	105	
CAT AGG ATC CAC TCA GTA CAA AGA ACA GAA CCC CTG GTG CTG TTC CGA His Arg Ile His Ser Val Gln Arg Thr Glu Pro Leu Val Leu Phe Arg 110 115 120 125			385
AGA GGC GCT GCT CGT GGG TTA GAG GCC TTG CTT GCA GAG CCA CAG CAG Arg Gly Ala Ala Arg Gly Leu Glu Ala Leu Leu Ala Glu Pro Gln Gln 130 135 140			433
AAC ATT GAA GCT GTC ATA CCA GAT GAG GAA GTG ATC GAG TGG TCA GAG Asn Ile Glu Ala Val Ile Pro Asp Glu Glu Val Ile Glu Trp Ser Glu 145 150 155			481
GTT TTC ATG TTA TTT AAG CAA CCG GTT TTA ATT TTT ATT ACT GAA AAT Val Phe Met Leu Phe Lys Gln Pro Val Leu Ile Phe Ile Thr Glu Asn 160 165 170			529
CAT GGG AGT TAT GTT GCT TAT GTA CAA TTG TGC AAA TCA CAC AGC TTA His Gly Ser Tyr Val Ala Tyr Val Gln Leu Cys Lys Ser His Ser Leu 175 180 185			577
AGC AAA TAC ATA CTC TTA CTT GGA AAA GAA GAA AAA TCT GCT AAA CCA Ser Lys Tyr Ile Leu Leu Gly Lys Glu Glu Lys Ser Ala Lys Pro 190 195 200 205			625
AAT TTT ACT GCA CGT GTG GAT GGG AAA TTC ATC TCC CTG GTG TCG CTA Asn Phe Thr Ala Arg Val Asp Gly Lys Phe Ile Ser Leu Val Ser Leu 210 215 220			673
GGC TCT GAT GGG TGT GTA TAT GGA ACC TTG GTA CCA ATA TAT TCA AGT Gly Ser Asp Gly Cys Val Tyr Gly Thr Leu Val Pro Ile Tyr Ser Ser 225 230 235			721
GAC ACG GAA AAC AAT CAG AGG TTA GTT AGA GCA TTG ATG CTC AAG ACG Asp Thr Glu Asn Asn Gln Arg Leu Val Arg Ala Leu Met Leu Lys Thr 240 245 250			769
GTT GTG TCT GGC AGT GCT CGA AAT GGT TCT GCC CTC ACC ATC CTG GAT Val Val Ser Gly Ser Ala Arg Asn Gly Ser Ala Leu Thr Ile Leu Asp 255 260 265			817
CAA GAC CAC ATA GCA GTC CTG GGA CCT CCA CTT CCA GCT TCT AAG GAA Gln Asp His Ile Ala Val Leu Gly Pro Pro Leu Pro Ala Ser Lys Glu 270 275 280 285			865
TGC CTC TCC ATA TGG AAC ATA AAA TTT CAG ACA TTA CAG ACA TCA AAA Cys Leu Ser Ile Trp Asn Ile Lys Phe Gln Thr Leu Gln Thr Ser Lys 290 295 300			913
GAG CTG CCA CAA GGA ACC AGT GGG CAA CTC TGG TAT CAT GGG GAA ATA Glu Leu Pro Gln Gly Thr Ser Gly Gln Leu Trp Tyr His Gly Glu Ile 305 310 315			961
CTA TTT ATG CGA CAT GGG AAA AGT CTA ACT GTG ATT CCA TAC AAG TGC Leu Phe Met Arg His Gly Lys Ser Leu Thr Val Ile Pro Tyr Lys Cys 320 325 330			1009
GAA GCA TCA TCT CTG GCG AGC GCT CTT GGG AAG CTC AAG CAT ACT CAA Glu Ala Ser Ser Leu Ala Ser Ala Leu Gly Lys Leu Lys His Thr Gln 335 340 345			1057
GAG TCA GGC AGT CAT TCC GTG CCC CAT TTT GTA AAC TGG GAG ACG TGT			1105

Glu 350	Ser	Gly	Ser	His	Ser 355	Val	Pro	His	Phe	Val 360	Asn	Trp	Glu	Thr	Cys 365	
TCA	GAA	TAT	GAA	CTT	GGG	TCC	TAC	AGT	GCA	AAG	CAG	ACA	AGA	ACT	CTT	1153
Ser	Glu	Tyr	Glu	Leu	Gly	Ser	Tyr	Ser	Ala	Lys	Gln	Thr	Arg	Thr	Leu	
				370					375					380		
AGA	AAA	AAA	ACT	GAA	ACA	AAT	TTA	CAC	CCA	GAA	GTT	CCA	GGA	GTC	AAA	1201
Arg	Lys	Lys	Thr	Glu	Thr	Asn	Leu	His	Pro	Glu	Val	Pro	Gly	Val	Lys	
			385					390					395			
GAA	CTT	TTA	TCA	ATA	ATA	AAG	AAA	GAT	TCA	GAA	AAG	CAC	ATT	GAA	GTA	1249
Glu	Leu	Leu	Ser	Ile	Ile	Lys	Lys	Asp	Ser	Glu	Lys	His	Ile	Glu	Val	
		400					405					410				
GAA	CTA	CGT	AAG	TTT	TTG	GCT	AAG	TCG	ACA	CCT	GAC	TTT	CAT	ACT	ATA	1297
Glu	Leu	Arg	Lys	Phe	Leu	Ala	Lys	Ser	Thr	Pro	Asp	Phe	His	Thr	Ile	
	415					420					425					
ATT	GGA	GAC	ATA	GTG	TCT	GGA	CTT	CTG	GGA	AGA	TGT	AAA	GTG	GAA	CCA	1345
Ile	Gly	Asp	Ile	Val	Ser	Gly	Leu	Leu	Gly	Arg	Cys	Lys	Val	Glu	Pro	
430					435					440					445	
TCG	TTT	TAC	CCC	CGG	AAC	TGT	CTG	ATG	CAG	CTC	ATC	CAG	ACA	CAC	GTG	1393
Ser	Phe	Tyr	Pro	Arg	Asn	Cys	Leu	Met	Gln	Leu	Ile	Gln	Thr	His	Val	
				450					455					460		
CTT	TCC	TAC	AGC	TTA	TGC	CCT	GAC	TTG	ATG	GAG	ATT	GCC	CTA	GAG	CAC	1441
Leu	Ser	Tyr	Ser	Leu	Cys	Pro	Asp	Leu	Met	Glu	Ile	Ala	Leu	Glu	His	
			465				470					475				
ACA	GAT	GTG	CAG	ATG	TTA	CAG	CTG	TGT	CTG	CAG	CAG	TTC	CCT	GAC	ATT	1489
Thr	Asp	Val	Gln	Met	Leu	Gln	Leu	Cys	Leu	Gln	Gln	Phe	Pro	Asp	Ile	
		480				485						490				
CCT	GAG	TCC	ACC	ACC	TGT	GCT	TGC	TTA	AAA	CTT	TTC	CTG	AGC	ATT	GGT	1537
Pro	Glu	Ser	Thr	Thr	Cys	Ala	Cys	Leu	Lys	Leu	Phe	Leu	Ser	Ile	Gly	
	495				500						505					
GAT	GAC	TGT	CTT	CGG	GAC	AGT	AAT	GTC	AGC	ATG	GAG	TCA	GTT	TTT	GAT	1585
Asp	Asp	Cys	Leu	Arg	Asp	Ser	Asn	Val	Ser	Met	Glu	Ser	Val	Phe	Asp	
510					515					520					525	
TAT	GGT	GAT	ACT	ACA	CAA	GAT	GAG	AAA	AAG	GAA	ATG	GAA	GAG	CAA	ACT	1633
Tyr	Gly	Asp	Thr	Thr	Gln	Asp	Glu	Lys	Lys	Glu	Met	Glu	Glu	Gln	Thr	
				530				535						540		
GAA	ATT	GTT	CAG	AAT	GGC	TTC	GGT	CCT	GAA	GAT	GGT	GGC	TGC	AGT	AAA	1681
Glu	Ile	Val	Gln	Asn	Gly	Phe	Gly	Pro	Glu	Asp	Gly	Gly	Cys	Ser	Lys	
			545					550					555			
GAT	AGT	CAG	CAG	TTG	AAC	AAA	AAG	CCT	GGT	GAC	ACA	GCA	CAG	GAG	CCC	1729
Asp	Ser	Gln	Gln	Leu	Asn	Lys	Lys	Pro	Gly	Asp	Thr	Ala	Gln	Glu	Pro	
		560					565					570				
ATC	TCC	TTC	CCT	GTG	ACC	TTG	TGT	CCT	GTG	GCA	CCA	AAG	CGA	GCA	GCT	1777
Ile	Ser	Phe	Pro	Val	Thr	Leu	Cys	Pro	Val	Ala	Pro	Lys	Arg	Ala	Ala	
	575					580					585					
CTG	CTA	AAT	GCA	GTC	CTT	CAT	TCA	GCA	TAC	AGT	GAG	CCC	TTC	CTC	CTG	1825
Leu	Leu	Asn	Ala	Val	Leu	His	Ser	Ala	Tyr	Ser	Glu	Pro	Phe	Leu	Leu	
590					595					600					605	

CCG CAC TTG AAG GAC ATC CCT GCG AAG CAT ATA ACG CTG TTT CTG CAG Pro His Leu Lys Asp Ile Pro Ala Lys His Ile Thr Leu Phe Leu Gln 610 615 620	1873
TAT TTG TAT TTC CTC TAT TTG AAG TGC ACT GGC AGT GCT ACC ATG ACT Tyr Leu Tyr Phe Leu Tyr Leu Lys Cys Thr Gly Ser Ala Thr Met Thr 625 630 635	1921
CTC CCT GGA GTA AGC CCT CCA ACC GTG AGC CAG ATC ATG GAT TGG ATA Leu Pro Gly Val Ser Pro Pro Thr Val Ser Gln Ile Met Asp Trp Ile 640 645 650	1969
TGC CTA CTT CTA GAT GCT AAT TTT ACT GTC GTC TTA ATG ATA CCA GAA Cys Leu Leu Leu Asp Ala Asn Phe Thr Val Val Leu Met Ile Pro Glu 655 660 665	2017
GCA AAA AGA CTT TTG CTT AAT CTT TAC AAT TTT GTG AAA TCG CAG ATC Ala Lys Arg Leu Leu Leu Asn Leu Tyr Asn Phe Val Lys Ser Gln Ile 670 675 680 685	2065
TCC ATC TAC TCC GAG CTC AAC AAG ATT GAA GTC AGC TTC CGG GAG CTG Ser Ile Tyr Ser Glu Leu Asn Lys Ile Glu Val Ser Phe Arg Glu Leu 690 695 700	2113
CAG AGG TTA AAT CAG GAG AAG AGC AGT AGA GGA CTG TAC TCC ATC GAA Gln Arg Leu Asn Gln Glu Lys Ser Ser Arg Gly Leu Tyr Ser Ile Glu 705 710 715	2161
GTT CTG GAA CTT TTC TGACAGCCAG AGACAGTCTT ACTGGTTGTC CTAGAACTGG Val Leu Glu Leu Phe 720	2216
ATATATAGAC CAAGCTGGCC TCAAACCTCAC AGAGATCCAA CCCAGAGCAC TGCATTAAA	2276
GGTGTGGCCA CCACACCTGG CTTAATGGAT TTTTTTATAT GAATGTACCT GTTCATCCAG	2336
GGGAGAAAGT TTGTGTTGTA TCCATCTCAG TGTCCAGAGA GGAGTGTGAG TCTCTGCACC	2396
ATCACATACC ACCATTCCCTC AGTGCTACGG GTTCCACAGA CATCACTTCT GGGTTGCAGA	2456
CATCACTGGA AGAATGTTAC AAACCTTTTAA AACATGGAAT TGAGTTGATT TTAAGTAAAC	2516
TTATTTGTGT ACTGATAAAA A	2537

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 722 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ala	Ala	Leu	Glu	Glu	Glu	Phe	Thr	Leu	Ser	Thr	Gly	Val	Leu	Gly
1				5					10					15	
Ala	Gly	Pro	Glu	Gly	Phe	Leu	Gly	Val	Glu	Pro	Ser	Asp	Lys	Ala	Asp
			20					25					30		
Gln	Phe	Leu	Val	Thr	Asp	Arg	Gly	Arg	Thr	Val	Val	Leu	Tyr	Lys	Val

35					40					45					
Ser	Asp	Gln	Lys	Pro	Leu	Gly	Ser	Trp	Ser	Val	Lys	Gln	Gly	Gln	Thr
50					55					60					
Ile	Thr	Cys	Pro	Ala	Val	Cys	Asn	Phe	Gln	Thr	Gly	Glu	Tyr	Ile	Met
65					70					75					80
Val	His	Asp	His	Lys	Val	Leu	Arg	Ile	Trp	Asn	Asn	Glu	Asp	Val	Asn
				85					90					95	
Leu	Asp	Lys	Val	Phe	Lys	Ala	Thr	Leu	Ser	Ala	Glu	Val	His	Arg	Ile
			100					105					110		
His	Ser	Val	Gln	Arg	Thr	Glu	Pro	Leu	Val	Leu	Phe	Arg	Arg	Gly	Ala
		115					120					125			
Ala	Arg	Gly	Leu	Glu	Ala	Leu	Leu	Ala	Glu	Pro	Gln	Gln	Asn	Ile	Glu
		130				135					140				
Ala	Val	Ile	Pro	Asp	Glu	Glu	Val	Ile	Glu	Trp	Ser	Glu	Val	Phe	Met
145					150					155					160
Leu	Phe	Lys	Gln	Pro	Val	Leu	Ile	Phe	Ile	Thr	Glu	Asn	His	Gly	Ser
			165						170					175	
Tyr	Val	Ala	Tyr	Val	Gln	Leu	Cys	Lys	Ser	His	Ser	Leu	Ser	Lys	Tyr
			180					185					190		
Ile	Leu	Leu	Leu	Gly	Lys	Glu	Glu	Lys	Ser	Ala	Lys	Pro	Asn	Phe	Thr
		195					200					205			
Ala	Arg	Val	Asp	Gly	Lys	Phe	Ile	Ser	Leu	Val	Ser	Leu	Gly	Ser	Asp
		210				215					220				
Gly	Cys	Val	Tyr	Gly	Thr	Leu	Val	Pro	Ile	Tyr	Ser	Ser	Asp	Thr	Glu
225					230					235					240
Asn	Asn	Gln	Arg	Leu	Val	Arg	Ala	Leu	Met	Leu	Lys	Thr	Val	Val	Ser
				245					250					255	
Gly	Ser	Ala	Arg	Asn	Gly	Ser	Ala	Leu	Thr	Ile	Leu	Asp	Gln	Asp	His
			260				265						270		
Ile	Ala	Val	Leu	Gly	Pro	Pro	Leu	Pro	Ala	Ser	Lys	Glu	Cys	Leu	Ser
		275					280					285			
Ile	Trp	Asn	Ile	Lys	Phe	Gln	Thr	Leu	Gln	Thr	Ser	Lys	Glu	Leu	Pro
	290				295					300					
Gln	Gly	Thr	Ser	Gly	Gln	Leu	Trp	Tyr	His	Gly	Glu	Ile	Leu	Phe	Met
305				310						315					320
Arg	His	Gly	Lys	Ser	Leu	Thr	Val	Ile	Pro	Tyr	Lys	Cys	Glu	Ala	Ser
				325					330					335	
Ser	Leu	Ala	Ser	Ala	Leu	Gly	Lys	Leu	Lys	His	Thr	Gln	Glu	Ser	Gly
			340					345				350			
Ser	His	Ser	Val	Pro	His	Phe	Val	Asn	Trp	Glu	Thr	Cys	Ser	Glu	Tyr
		355					360					365			
Glu	Leu	Gly	Ser	Tyr	Ser	Ala	Lys	Gln	Thr	Arg	Thr	Leu	Arg	Lys	Lys

370					375					380						
Thr	Glu	Thr	Asn	Leu	His	Pro	Glu	Val	Pro	Gly	Val	Lys	Glu	Leu	Leu	
385					390					395					400	
Ser	Ile	Ile	Lys	Lys	Asp	Ser	Glu	Lys	His	Ile	Glu	Val	Glu	Leu	Arg	
			405						410					415		
Lys	Phe	Leu	Ala	Lys	Ser	Thr	Pro	Asp	Phe	His	Thr	Ile	Ile	Gly	Asp	
			420					425					430			
Ile	Val	Ser	Gly	Leu	Leu	Gly	Arg	Cys	Lys	Val	Glu	Pro	Ser	Phe	Tyr	
		435					440					445				
Pro	Arg	Asn	Cys	Leu	Met	Gln	Leu	Ile	Gln	Thr	His	Val	Leu	Ser	Tyr	
	450					455					460					
Ser	Leu	Cys	Pro	Asp	Leu	Met	Glu	Ile	Ala	Leu	Glu	His	Thr	Asp	Val	
465					470					475					480	
Gln	Met	Leu	Gln	Leu	Cys	Leu	Gln	Gln	Phe	Pro	Asp	Ile	Pro	Glu	Ser	
			485						490					495		
Thr	Thr	Cys	Ala	Cys	Leu	Lys	Leu	Phe	Leu	Ser	Ile	Gly	Asp	Asp	Cys	
			500					505					510			
Leu	Arg	Asp	Ser	Asn	Val	Ser	Met	Glu	Ser	Val	Phe	Asp	Tyr	Gly	Asp	
		515					520					525				
Thr	Thr	Gln	Asp	Glu	Lys	Lys	Glu	Met	Glu	Glu	Gln	Thr	Glu	Ile	Val	
		530					535					540				
Gln	Asn	Gly	Phe	Gly	Pro	Glu	Asp	Gly	Gly	Cys	Ser	Lys	Asp	Ser	Gln	
545					550					555					560	
Gln	Leu	Asn	Lys	Lys	Pro	Gly	Asp	Thr	Ala	Gln	Glu	Pro	Ile	Ser	Phe	
			565						570					575		
Pro	Val	Thr	Leu	Cys	Pro	Val	Ala	Pro	Lys	Arg	Ala	Ala	Leu	Leu	Asn	
			580					585					590			
Ala	Val	Leu	His	Ser	Ala	Tyr	Ser	Glu	Pro	Phe	Leu	Leu	Pro	His	Leu	
		595					600					605				
Lys	Asp	Ile	Pro	Ala	Lys	His	Ile	Thr	Leu	Phe	Leu	Gln	Tyr	Leu	Tyr	
	610					615					620					
Phe	Leu	Tyr	Leu	Lys	Cys	Thr	Gly	Ser	Ala	Thr	Met	Thr	Leu	Pro	Gly	
625					630					635					640	
Val	Ser	Pro	Pro	Thr	Val	Ser	Gln	Ile	Met	Asp	Trp	Ile	Cys	Leu	Leu	
				645					650					655		
Leu	Asp	Ala	Asn	Phe	Thr	Val	Val	Leu	Met	Ile	Pro	Glu	Ala	Lys	Arg	
			660					665					670			
Leu	Leu	Leu	Asn	Leu	Tyr	Asn	Phe	Val	Lys	Ser	Gln	Ile	Ser	Ile	Tyr	
		675					680					685				
Ser	Glu	Leu	Asn	Lys	Ile	Glu	Val	Ser	Phe	Arg	Glu	Leu	Gln	Arg	Leu	
	690					695					700					
Asn	Gln	Glu	Lys	Ser	Ser	Arg	Gly	Leu	Tyr	Ser	Ile	Glu	Val	Leu	Glu	

705

710

715

720

Leu Phe

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW016

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 385..748
- (D) OTHER INFORMATION: /label= SAC_24530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATTATTCTCC CCTGTGTCATT AAAAGAAATC AGCAAAACCA AACAACTGGC TACACCACGA	60
ATTGTCGTTA AATTGCTAA CTGGTGCTA AAAGCCGTGT AGCTACCTCG GTCCTGCTTG	120
CTAGGTTTGC CACTAGAAGG AAGCATACTT AAAACAATGG CTACTTGGAT CCTCAGGGAG	180
ATCCTGTCTG CAGTCGCGTG GTCACCCTTA GCTTCATCAA AGCACTAACA GCTCACCCGG	240
CCAGGCTTCA TGAGCACTGA CCCTCAAGCA AGCAGGTTTA TTAAACATTT AGATGCCAAC	300
CTCACTTACT GTTTCCTGCA GTCATGGAGA GTTFACTTAA CAAGTTTGTA AATAATAAAC	360
TGGCACTTTG CACACAGACT TGGTACTATC CTAGGGGAAG GCCTGCTTTA TTTGGTTTCT	420
AGACCGAGTA GGAAGTGATC CATTTACCAC TGAGGGCAGC CCCATTGAGA GTCTTAAGTG	480
ACTAAGCCAG TGTTGAACAA GCAATTTCCA GGCTTTGTTC TTCAGGGAAC TTCCCATCAG	540
CTTTGAAGTC GGTCTGTGTC ACCCTAGGCA CATGGATCAG TTCACAAGTG GGGTTCAGTG	600
GAGAGAACTT CCCCCTCAGA AGTCACTTGA AACTTAGATG AGATTTGGGA CACTTGCTGG	660
TTGACTCTGT CTCATTGTG TAAAAAGTAG TTTNTNTNAA NANINGGTTT TTTTTTTTTT	720
TTCAAGGTTA TACTTTGTCC CATTCCTANG TTANTACAAA GTCTTGAAAG GGCCTTTGTA	780
GGGCTTTTTA ANNCAGGGTC TTAACATGT AACTCTGGCT TGGCCTGGAA CTGCTATGT	840
AGACCAGGTT ACCCTCAAAC TTGCCTGTCT TCCCAAATAC TGGGATTAAG GTTCTGTGA	900
CCATACCTGG CTTTACCTGA TGAATTCCTA AACACCAGAA AACCAGTACT GTATGAGATG	960

TTAATGTGTG TTCCTTTCAG ACTGGAGTAC AGACCAGTAG ATAACAGATA ACAGCTGGTT	1020
CACCTTAATC TGCCTTTTTG TGTATTAATC TGTGTTTAGA GAACGGAACA ATAGCCAGAA	1080
TTNNCTAGC GAGTTCGAGG CCAGTTGGTG TATATGTGGG ACTCTTAACC AAAACAGCAA	1140
GCGTTCCTG GGGTAGTTCA CAATGATCTC CAGCTTCCTT GTTAACCAGA TAACTGCNAN	1200
TCCAGATGTA TGACCCTGGT TGGTTTATG TATTGATATG TTTCTGTAAT ATGAGTAAAT	1260
TATTGTTACT TAAAAGTAAT AAATTCAAGT TTCAAAATG AAAAA	1305

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 955 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: HW017
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION: 393..627
 - (D) OTHER INFORMATION: /label= SAC_24091

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTGACAATC CTGTTATGAC AAGCCCGTCT CGATACTGAC AACTGAAGTG GAAATTGCTT	60
GAACATCAAG ATAGCTAACT CGGAAAGAAT CCCAGACTTT GGATAGTTTC TGAGTCTTCT	120
AGAATTTTCC AAGAAGAAAC CATGGTGGCA AATGCGGAGA CTCGGGCGGG CACTGGGAAC	180
ACAGCACAGT GGTCCTTAGGG AGGTGCTTTG TCAGGAATGA ACAGTCATGG TTATAATCCA	240
CGTTTCCATT GCTACTCAGC AATGATCTC TTTCTGTTTG TTTTAAAAT TTTTACAC	300
TGAATTTCTA TTTAGACACT AAAACATATA GGGGTGCTTG TCACCCGGAT ACATTTATCT	360
GTGAGCCAGC TATTCGGATG TCATGGCTGG GTACCTAACT TACTTCCATA TGTGAAGTGT	420
GCTAAACTCA AACCAGTTTA CAGAAACGAT GTATTTTGTG TATAGTAAAT TGTATATTCA	480
CCCTTTTACC ACGGCCGGTT TTTTAAACAA ATGAATACTC TAGATTTTTC TTCCAAATGA	540
GGTTACTGTT GGGGTGGGGT TGACTTAGTG ATGCTGTAGA AGGGAATCCG CATGCACTAA	600
AAAGTGTGTC TGCCTAAAAG TGTGTACAGC AGGCACAACC TTCCTTGTGG ATTTCCGTCT	660
GCTCACTGCA GATCTGCCTG TGGTTTAGAA ATAGAATTCA AGAGCCATCA AGGAGTGACC	720
AGCTTGACAC CACTGCCAAA TTCAGAATGA GGAACCTTGA GAGAAGGAAC TGTCGCTCAG	780
CCAGAAGCAG ATGAAGCCAC TGGTCCTGGT TCACAGTTTA GTGTCATGCT CTGGTTTATA	840

AGGATGGGCA TTACGTTCCG TGTATCTGG TTATCTGCGA GATTCTAAAC CGAGGTGCAA 900
GAGCTCCTAT CCTGATTCTG AGATTTGAAA TAAAGCATGA ATGAACAAAG AAAAA 955

(2) INFORMATION FOR SEQ ID NO:13:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1198 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:
 (B) CLONE: HW018

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 86..1102
 (D) OTHER INFORMATION: /product= "predicted polypeptide"

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION: complement (644..994)
 (D) OTHER INFORMATION: /label= SAC_23880
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

|                                                                   |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
|-------------------------------------------------------------------|-----|--|--|--|--|--|--|--|--|--|--|--|--|-----|
| GTCGACCTGG GAGTCCGGGC AGCGAGCCCC TCGCCGTCGG GTCCCACGAA GAAACTGGTG |     |  |  |  |  |  |  |  |  |  |  |  |  | 60  |
| GCTGAAGCCA TATTCTGCAG CATTCT ATG GAG ATC AGT AAA AAT ATT ACG AAC  |     |  |  |  |  |  |  |  |  |  |  |  |  | 112 |
| Met Glu Ile Ser Lys Asn Ile Thr Asn                               |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| 1 5                                                               |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| CCA GAA GAA CTT TGG AAA ATG AAG CCT AAG GGG AAC CTG GAA GAT GAC   | 160 |  |  |  |  |  |  |  |  |  |  |  |  |     |
| Pro Glu Glu Leu Trp Lys Met Lys Pro Lys Gly Asn Leu Glu Asp Asp   |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| 10 15 20 25                                                       |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| AGT TAC TCG ACT AAG GAC ACC GGA GAG ACA AGC ATG CTG AAA AGA CCG   | 208 |  |  |  |  |  |  |  |  |  |  |  |  |     |
| Ser Tyr Ser Thr Lys Asp Thr Gly Glu Thr Ser Met Leu Lys Arg Pro   |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| 30 35 40                                                          |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| GTG CTC TCG CCT TTG CCG CAC ACG GTC CAC GTC GAC GCC TTC GAC TGC   | 256 |  |  |  |  |  |  |  |  |  |  |  |  |     |
| Val Leu Ser Pro Leu Pro His Thr Val His Val Asp Ala Phe Asp Cys   |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| 45 50 55                                                          |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| CCC ACG GAG CTC CAG CAC ACG CAG GAA CTC TTT CCA AAC TGG CAA TTG   | 304 |  |  |  |  |  |  |  |  |  |  |  |  |     |
| Pro Thr Glu Leu Gln His Thr Gln Glu Leu Phe Pro Asn Trp Gln Leu   |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| 60 65 70                                                          |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| CCA ATT AAA GTT GCC GCC GTC CTA TCG TCT CTC ACC TTC CTG TAC ACT   | 352 |  |  |  |  |  |  |  |  |  |  |  |  |     |
| Pro Ile Lys Val Ala Ala Val Leu Ser Ser Leu Thr Phe Leu Tyr Thr   |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| 75 80 85                                                          |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| CTT CTG AGG GAA ATC ATT TAC CCA TTA GTC GCT TCC CGC GAA CAG TAT   | 400 |  |  |  |  |  |  |  |  |  |  |  |  |     |
| Leu Leu Arg Glu Ile Ile Tyr Pro Leu Val Ala Ser Arg Glu Gln Tyr   |     |  |  |  |  |  |  |  |  |  |  |  |  |     |
| 90 95 100 105                                                     |     |  |  |  |  |  |  |  |  |  |  |  |  |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| TTT TAT AAG ATC CCG ATC CTG GTC GTT AAC AAA GTC TTG CCA ATG GTC<br>Phe Tyr Lys Ile Pro Ile Leu Val Val Asn Lys Val Leu Pro Met Val<br>110 115 120     | 448  |
| TCC ATT ACC CTC TTG GCA TTG GTT TAT CTG CCA GGA GAG ATA GCG GCA<br>Ser Ile Thr Leu Leu Ala Leu Val Tyr Leu Pro Gly Glu Ile Ala Ala<br>125 130 135     | 496  |
| GTT GTG CAG CTT CGC AAT GGG ACC AAG TAC AAG AAG TTC CCA CCC TGG<br>Val Val Gln Leu Arg Asn Gly Thr Lys Tyr Lys Lys Phe Pro Pro Trp<br>140 145 150     | 544  |
| TTA GAC AGA TGG ATG CTG GCG AGG AAA CAA TTT GGG CTC CTC AGC TTC<br>Leu Asp Arg Trp Met Leu Ala Arg Lys Gln Phe Gly Leu Leu Ser Phe<br>155 160 165     | 592  |
| TTC TTT GCA GTT CTG CAC GCC ATT TAC AGT CTC TCG TAC CCA ATG AGA<br>Phe Phe Ala Val Leu His Ala Ile Tyr Ser Leu Ser Tyr Pro Met Arg<br>170 175 180 185 | 640  |
| CGG TCC TAC AGA TAC AAG CTG CTC AAC TGG GCT TAC AAA CAG GTT CAA<br>Arg Ser Tyr Arg Tyr Lys Leu Leu Asn Trp Ala Tyr Lys Gln Val Gln<br>190 195 200     | 688  |
| CAA AGC AAA GAA GAT GCC TGG GTT GAG CAT GAT GTC TGG AGA ATG GAG<br>Gln Ser Lys Glu Asp Ala Trp Val Glu His Asp Val Trp Arg Met Glu<br>205 210 215     | 736  |
| ATT TAT GTG TCC CTG GGG ATT GTG GGA CTG GCC ATC TTG GCT CTC TTG<br>Ile Tyr Val Ser Leu Gly Ile Val Gly Leu Ala Ile Leu Ala Leu Leu<br>220 225 230     | 784  |
| GCT GTG ACA TCT ATC CCA TCT GTG AGC GAC TCT TTA ACC TGG AGA GAA<br>Ala Val Thr Ser Ile Pro Ser Val Ser Asp Ser Leu Thr Trp Arg Glu<br>235 240 245     | 832  |
| TTT CAC TAT ATT CAG AGC AAA CTG GGA ATT GTC TCT CTT CTT CTG GGC<br>Phe His Tyr Ile Gln Ser Lys Leu Gly Ile Val Ser Leu Leu Leu Gly<br>250 255 260 265 | 880  |
| ACG GTA CAC GCT TCG ATT TTT GCC TGG AAT AAA TGG GTA GAT ATC AGT<br>Thr Val His Ala Ser Ile Phe Ala Trp Asn Lys Trp Val Asp Ile Ser<br>270 275 280     | 928  |
| CAG TTT GTC TGG TAC ATG CCT CCG ACT TTC ATG ATA GCT GTT TTC CTT<br>Gln Phe Val Trp Tyr Met Pro Pro Thr Phe Met Ile Ala Val Phe Leu<br>285 290 295     | 976  |
| CCA ACT GTT GTT CTG ATC TGT AAA ATT GTA CTT TGC CTG CCC TGC CTG<br>Pro Thr Val Val Leu Ile Cys Lys Ile Val Leu Cys Leu Pro Cys Leu<br>300 305 310     | 1024 |
| AGG AAG AAG ATA CTG AAG ATT AGA TGT GGT TGG GAA GAT GTC CGC AAA<br>Arg Lys Lys Ile Leu Lys Ile Arg Cys Gly Trp Glu Asp Val Arg Lys<br>315 320 325     | 1072 |
| GTT AAC AGG ACT GAG ATG GCC TGC AGG TTG TAGAACTACT GTTTGCACAT<br>Val Asn Arg Thr Glu Met Ala Cys Arg Leu<br>330 335                                   | 1122 |
| AATTGCTTAA TACCGATGTC TTATAAACAT TTCAAACCTG TGTCTGTTAA TAAAATGAAT                                                                                     | 1182 |

ACTTCTGGAT CAAAAA

1198

## (2) INFORMATION FOR SEQ ID NO:14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

Met Glu Ile Ser Lys Asn Ile Thr Asn Pro Glu Glu Leu Trp Lys Met
 1 5 10 15
Lys Pro Lys Gly Asn Leu Glu Asp Asp Ser Tyr Ser Thr Lys Asp Thr
 20 25 30
Gly Glu Thr Ser Met Leu Lys Arg Pro Val Leu Ser Pro Leu Pro His
 35 40 45
Thr Val His Val Asp Ala Phe Asp Cys Pro Thr Glu Leu Gln His Thr
 50 55 60
Gln Glu Leu Phe Pro Asn Trp Gln Leu Pro Ile Lys Val Ala Ala Val
 65 70 75 80
Leu Ser Ser Leu Thr Phe Leu Tyr Thr Leu Leu Arg Glu Ile Ile Tyr
 85 90 95
Pro Leu Val Ala Ser Arg Glu Gln Tyr Phe Tyr Lys Ile Pro Ile Leu
 100 105 110
Val Val Asn Lys Val Leu Pro Met Val Ser Ile Thr Leu Leu Ala Leu
 115 120 125
Val Tyr Leu Pro Gly Glu Ile Ala Ala Val Val Gln Leu Arg Asn Gly
 130 135 140
Thr Lys Tyr Lys Lys Phe Pro Pro Trp Leu Asp Arg Trp Met Leu Ala
 145 150 155 160
Arg Lys Gln Phe Gly Leu Leu Ser Phe Phe Phe Ala Val Leu His Ala
 165 170 175
Ile Tyr Ser Leu Ser Tyr Pro Met Arg Arg Ser Tyr Arg Tyr Lys Leu
 180 185 190
Leu Asn Trp Ala Tyr Lys Gln Val Gln Gln Ser Lys Glu Asp Ala Trp
 195 200 205
Val Glu His Asp Val Trp Arg Met Glu Ile Tyr Val Ser Leu Gly Ile
 210 215 220
Val Gly Leu Ala Ile Leu Ala Leu Leu Ala Val Thr Ser Ile Pro Ser
 225 230 235 240
Val Ser Asp Ser Leu Thr Trp Arg Glu Phe His Tyr Ile Gln Ser Lys
 245 250 255
Leu Gly Ile Val Ser Leu Leu Leu Gly Thr Val His Ala Ser Ile Phe

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|                                                                 |     |     |
|-----------------------------------------------------------------|-----|-----|
| 260                                                             | 265 | 270 |
| Ala Trp Asn Lys Trp Val Asp Ile Ser Gln Phe Val Trp Tyr Met Pro |     |     |
| 275                                                             | 280 | 285 |
| Pro Thr Phe Met Ile Ala Val Phe Leu Pro Thr Val Val Leu Ile Cys |     |     |
| 290                                                             | 295 | 300 |
| Lys Ile Val Leu Cys Leu Pro Cys Leu Arg Lys Lys Ile Leu Lys Ile |     |     |
| 305                                                             | 310 | 315 |
| 320                                                             |     |     |
| Arg Cys Gly Trp Glu Asp Val Arg Lys Val Asn Arg Thr Glu Met Ala |     |     |
| 325                                                             | 330 | 335 |
| Cys Arg Leu                                                     |     |     |

## (2) INFORMATION FOR SEQ ID NO:15:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1801 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: HW032

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: complement (1412..1793)
- (D) OTHER INFORMATION: /label= SAC\_24831

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TTTTTCCAGC TTTTAAAGTT GCATTTATTT TTGATAATCT GTACTGTAGC CAATCAATTC  | 60  |
| TATTCTCCAT TCTTGCTTAA TTGTATTAGC CATAAAGGAG TTCAGGTTCA TAGGACTCAG  | 120 |
| TTTCTCTATT AAACCGTCAT TGATTATGGA AATACTGTCT TAAGCACTAT GCAGATTAAC  | 180 |
| ACCATACTTT TCTTCCATTA CATCTTTCAA GACAGTCACT CACAACCTAG AAGACTGATA  | 240 |
| CAGCATTAGA TGAAAAAAC AAGATTCA CA GATATATGTA GTGAAACTCA AACTAGGAGT  | 300 |
| CTTAGAGATA AAAAAGATAA GTAGATATTT AAAATGTAGT CTGTTAAAGA TTTAATCGGT  | 360 |
| TTAAAGTATA AGATTAGAAA GACAAAGTTT CTATTGTTTT GAAAGTTTTA AGTAAAGAAA  | 420 |
| AAAAAACTGG AAAATATGTC TTTGTTGTTC TTTCTCCGTT CTTAATTACG AGCTATCCAA  | 480 |
| CAGAAACCCC TAGGTCATAG TTTATGTTTC TGTTCTCATC AATGTAAC TA GAACACTGGA | 540 |
| GAAAGAAAAA GGAAGACATA TTAACCAATG GCCGCAATCA CTTTTCACTT GCCCCACGGT  | 600 |
| ACAAATCTGA TTTGGATGAA ATGGTTTGTG GCATAAAAT TTTAAATTTT AGAAGCCAAT   | 660 |

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GTGGTAGATT TCTCCATGTT TGCACAAATC CAATTTCAAC TACTTTTACT TCACTAATTA 720
ATTAAATGGA TTGGAAACAT TCTAGAAATG AAATTGTGTC TTTAGATGGA GTTGGGGAGA 780
GTACGCTTTA TTTTAAATAT TTAGTTCAAA TTTCATTTTC ACTTCTTGGT CTTATTATTT 840
CAGCTTCAGT TGGGGCTGGC TTCTGTGGGG CTTACATGCT GACTGTGTCA GGCAGCTGGA 900
GGTGATCTAC ATTGACAGGA TTCAATGACT TTCTCCTCCG CGAAAAGCCC CTGTCAGCTA 960
CACAAGGATG GGAGGTTTTC GGCACACTGT CAAGTGATTG CAGATCCTGA CTTCTCAAAT 1020
ATGAGGTGTC GGCAGTGGCA GCAGCAGCTA CTGGTAGCTG CCCCAGACTC CTCAGATAAC 1080
TTACACAGGA GCTGGTTTAT GCATCCCCCTT CGTCAGAGCT TCCTCTGGGC AAGTGAAAGT 1140
TGCAAGCCTT CACTTGCCCC CATGTCTCAG CTCTCTAAGT GACCCTGCCT GTGCTGGCCC 1200
TTGTGCTTAT GGTGGTGGTG GTGGTGGTGC AAGCCTGAAG GAGGAAGACT TGTCTCAACA 1260
TCTAATGCCC CTGGTTGCTG ATTCTCTGAA GGCTTACTGC TCCCAGCAAC CGTCAGCCTC 1320
AGTCGCAGCC GGGCCTCGCT CCTCAACTTG GCAAAAATGC CTACAGAGAC TGAGAGATGC 1380
ATCGAGTCCC TGATTGCTGT TTTCCAGAAG TACAGTGGGA AGGATGGAAA TAGCTGTCAT 1440
CTCTCCAAAA CTGAGTTCTT TTCCTTCATG AACACGGAGC TGGCCGCCCTT CACGAAGAAC 1500
CAGAAGGACC CCGGTGTCCT CGACCGCATG ATGAAGAAGC TGGACCTCAA CAGTGATGGG 1560
CAGCTAGATT TCCAAGAGTT TCTCAACCTT ATTGGTGGCT TAGCTATAGC ATGCCATGAG 1620
TCCTTCCTCC AGACTTCCCA GAAGCGTATC TAACCTCTC CATTCCTTTC CAGCCACCAA 1680
GTCATCGCCT CCTCCACTCC TTCCCCATC CACACCTGCA CTGAGCCCAC CACACCTACC 1740
ACACATGCAG CCCACGCCTG ACAGGGAAAA TAAAACAATG TCATTTTTTTT AAATGTAAAA 1800
A 1801

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## (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2646 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: HW033
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 50..263
  - (D) OTHER INFORMATION: /label= SAC\_23901
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

|            |            |             |            |             |             |      |
|------------|------------|-------------|------------|-------------|-------------|------|
| GTCGACTTGA | CTTCTTAGTT | TTCTGACGGG  | AGCTCTCTTC | CTTCTGAGTA  | CTAGTCTCGG  | 60   |
| GCCTCCAGCC | CCAGGAAGAC | CCTCTGCTTT  | TCTCTCCACC | CTTGGCTTGC  | TCCTCAGCAG  | 120  |
| GGAAGAAGTA | GATCACAGTC | TCACTGCCTT  | CAGTTCCCAG | CTTTGCCAGT  | CACCAGCTGT  | 180  |
| GTAGTCTCAG | GCCAATCACC | ACCTCCTCTA  | GCCTAGGTAG | TTGGTTTTAT  | GTGGGTGAAT  | 240  |
| GTTTTGCCTG | GATGTATGTA | TGTACACCAC  | CTGTGTGCCT | GGTGCCCTG   | CAGTCAGAAG  | 300  |
| AAAGTGCCAC | ACCCCTAGGA | ACTGGAGTTA  | AGATGGGTTA | GAGCCTCCAT  | GTGGGTGCTG  | 360  |
| AGAACTGAAC | CTGGTTCTCT | GGAAAAGCAG  | CCGGCACTCA | ACCTCTGAGC  | CAGCTCTTCA  | 420  |
| TCCCCGAGTC | CGTTTATTTA | ACCGGCTATA  | AAATGGATT  | AAAACGACTT  | ACCTCACCAG  | 480  |
| GCCTGTGAAA | CATTTAAAAA | CTTAATAAAA  | ATTCTACACT | TAATTGTTTT  | TGCTTATGCT  | 540  |
| TTCTAGTCCC | TTAGTCTTA  | GACAGTTTCT  | GTTTCTTGTA | TTTATAAAGT  | TGGTATTAAA  | 600  |
| TATATAGCCA | GTGGACAAGA | ACCTTACTGC  | TATGGGCTGG | CCCCTGTAGG  | GTCTTAGACT  | 660  |
| AGAGGAGCGT | ACTTTGTGGT | TTAAAGTGGT  | TTGGCCTGCC | TACCTGTTTT  | TCCCCTGGA   | 720  |
| CTCAAAACAC | TAATAAAGCA | GGGGTGACCT  | GTGTCACCTG | AGCATTCAGC  | AGAACACTGG  | 780  |
| CCCAGGCAAT | GGCCTCAAAG | CTGGGCTACA  | TTATAAAGTG | AACTTTCTTG  | TTCATACTGG  | 840  |
| GTCACAGAAG | CAGGCCCAGA | AAAAATAAAA  | AATCCTGGTC | ACTCGGTTCC  | CCCTTGCACC  | 900  |
| ATCATCTGTT | CACTAGTGCC | CCTCTGACCA  | TTCTCACCCA | AGACAGGCAT  | CCTCTGGGAA  | 960  |
| CCTTAGGCAG | GTCCATTTCT | TCTTTGTTCAT | TTGGAATGAA | GCACTAACAG  | CCCTGGGGTC  | 1020 |
| TCTGCCATTG | GCTTCCCAGA | GTTGTCCAAT  | GAGTTTTCGT | GAAGGAATCT  | GGGTTTATCT  | 1080 |
| TTCCCGGGCT | TCCTGCCCTG | TTAGCAGAAT  | TTCAAATAGC | AGATAATAGA  | TTCTGACCTG  | 1140 |
| TGAGGCCATT | TTTCTCTCAA | TCCCTTTCTT  | CTGAGACATT | AGCCTTGGGC  | ATGCAGCAGC  | 1200 |
| TGCGCACTGG | TTTCAGGGAG | GAAAGGGGTG  | AATGGTGAGC | GAAC TTGGCC | CTGTGGATGC  | 1260 |
| TAACTCCACT | GAGATGAAAA | CATGGGGGCT  | TTTCTCTGAA | GACGCAGGGC  | CGTGTAACA   | 1320 |
| TATGACTTTG | ACCATATTCT | CAGGTTTGGG  | GATGTGGGAA | GTTCCAGGAA  | CAGAAATCCC  | 1380 |
| CTGCTGAGTT | CTTGGGCACT | GTGGCTATTT  | GTTCCCATGA | GGACCTCTCC  | CTGCAGTCTG  | 1440 |
| CCCTCTGGCA | GGGTGGAGTA | TAGAAGACTC  | AAGAGCTACA | GATGCCCCCG  | TCACTGGAGC  | 1500 |
| TCCCCTGCAC | CTAGGCCATC | AATCACGTCC  | ACCATCACCA | GAGGGGCTTA  | GGCCTAGGGT  | 1560 |
| GTATGCTGAG | GGAAAGACGA | GGGCCTGTCC  | CACTACTCGA | GTAGAGCAGA  | TGGCCTTCTG  | 1620 |
| TGTAGGCAGT | GAATTTTATA | GCAGTGCCTT  | GAGGAGCCCA | GCATGTTCTC  | AAGCACCTCC  | 1680 |
| TCCCAGTTTA | TATTTGGAAG | TCTGCTTCAC  | AGGGACCAGA | GGGCATAAAC  | CTAACCTACC  | 1740 |
| CACTTCCCAT | CAGGGACAGC | CCAAAGCACA  | CCAGTATATG | TAAGGGGTGC  | AGGGAGGTAT  | 1800 |
| CATGGGTCTC | TTCTCTCCTC | TCAGTGCTCA  | AACTCAGGTG | GAGGCTATGG  | ATT CAGGATC | 1860 |

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TTGGTTAGGA GTTGCAAGCA ATGGACAAGA AAGAGCATTA GGGAAACCAG AATCCCAGCC 1920
TGTCCCTGTG CCTCCACCCC AGCTAGACTT GAGGCTTAGG TCCTGATACT CTGCCCTTAC 1980
ACACCCTCTC TCCATTTCCC AGGAGTTAGT AAAAAACAGG CAAGGGTAAT ATGCTATCAT 2040
CTGTGGTCCT GAGCCTTCTC CAGACTTCCC CTTCACTCCG CCGCCACTGC CACCACCACA 2100
GAGACATCTT CGGAAGCATT AGGTTTATTT CTTGAACTGA ACTCCTGGGG AGAAGATGAC 2160
TGGTGCCACC ACATGTGCTC TGTCTGGTTA GGGGCCTTGA GGTGGCACAG TCCAGCCATA 2220
GAAGGATCAG CCTTCCTGCC CATAAGATT AATGCCAGG AGTCAGATAG TTGATGCGAC 2280
TGTAAGAGA AAGAGAGGTG AGATGGGGAC TCCAAGGTAC TGTAAGAGA AATCAAGTTT 2340
TTCTTCCCTA GCTCCATCCT CCACTCCAAA GCCTCAGGGA TCTGAAAACA GTCTTCATCC 2400
AGTCTATGTG CCCACAACCT TCAATGGTTC CCTACTTCCT CTTGTATATT TTTGGCTATT 2460
CTCTTCACCT CTAATTAGCT CATACTGTTT CCCACTGACT CCCGTCTTTA ATGGCTTCAT 2520
AGGTTTTCAG TCACGTATGA ATCTACACTG CATCACACAG TTACAAAACC CAGAGTTGGG 2580
GTTGGGGATT TAGCTCAGTG GCCTAGCAAG CGTAAGGCCC TGGGTTCCGT CCCCAGCCCC 2640
GAAAAA 2646

```

## (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4339 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: HW034
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 91..837
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 3101..4162
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 3561..3862
  - (D) OTHER INFORMATION: /label= SAC\_23897

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

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GTCGACGGAA GAGCTGTTGT GACTGCGGTA CTGCGGAGGG CTCTCGGCGG CCCGCGACAA 60
GGCTGAGTCC CGGGAGGTCC ATGCCCCACC ATG CTT TCC TGT GAC ATC TGT GGT 114

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| Met Leu Ser Cys Asp Ile Cys Gly |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|---------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| 15                              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| GAA                             | ACT | GTA | ACC | TCA | GAA | CCA | GAT | AGG | AAG | GCT | CAC | CTA | ATT | GTT | CAC | 162 |  |
| Glu                             | Thr | Val | Thr | Ser | Glu | Pro | Asp | Arg | Lys | Ala | His | Leu | Ile | Val | His |     |  |
| 10                              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| ATG                             | GAA | AAT | GAA | ATT | ATC | TGT | CCG | TTT | TGC | AAG | CTG | TCG | GGT | ATA | AAT | 210 |  |
| Met                             | Glu | Asn | Glu | Ile | Ile | Cys | Pro | Phe | Cys | Lys | Leu | Ser | Gly | Ile | Asn |     |  |
| 25                              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| TAC                             | AAT | GAA | ATG | TGT | TTT | CAT | ATT | GAA | ACC | GCT | CAT | TTT | GAA | CAG | ACT | 258 |  |
| Tyr                             | Asn | Glu | Met | Cys | Phe | His | Ile | Glu | Thr | Ala | His | Phe | Glu | Gln | Thr |     |  |
| 45                              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| ACG                             | CCA | GAA | AAA | AGC | TTC | GAG | ACG | CTA | GCC | GCA | GTG | CAA | TAT | GAA | AAT | 306 |  |
| Thr                             | Pro | Glu | Lys | Ser | Phe | Glu | Thr | Leu | Ala | Ala | Val | Gln | Tyr | Glu | Asn |     |  |
| 60                              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| TCA                             | GAC | CTC | GGT | AAT | ACC | AAG | CTG | CAC | AGT | ACA | GTG | GAA | GTT | ACC | TCA | 354 |  |
| Ser                             | Asp | Leu | Gly | Asn | Thr | Lys | Leu | His | Ser | Thr | Val | Glu | Val | Thr | Ser |     |  |
| 75                              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| GGC                             | ATC | CAT | TCA | GCT | TGT | GCA | TCG | AAC | TTT | CCA | AAG | GAG | TCG | TCC | GAA | 402 |  |
| Gly                             | Ile | His | Ser | Ala | Cys | Ala | Ser | Asn | Phe | Pro | Lys | Glu | Ser | Ser | Glu |     |  |
| 90                              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| AGC                             | CTT | TCT | AAA | GAT | AGG | ACT | TTA | AAA | CAA | GAA | GCT | TTT | TAT | ACA | GAG | 450 |  |
| Ser                             | Leu | Ser | Lys | Asp | Arg | Thr | Leu | Lys | Gln | Glu | Ala | Phe | Tyr | Thr | Glu |     |  |
| 105                             |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| AGC                             | GTA | GCT | GAA | TCT | AGA | AAG | TAC | CAG | AAA | AGC | AGA | GAA | AAG | CAG | TCC | 498 |  |
| Ser                             | Val | Ala | Glu | Ser | Arg | Lys | Tyr | Gln | Lys | Ser | Arg | Glu | Lys | Gln | Ser |     |  |
| 125                             |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| GGA                             | TTG | TCT | GAG | GCC | CAA | GGA | TCA | ATT | TAT | GAA | ACA | ACA | TAC | AGT | CCC | 546 |  |
| Gly                             | Leu | Ser | Glu | Ala | Gln | Gly | Ser | Ile | Tyr | Glu | Thr | Thr | Tyr | Ser | Pro |     |  |
| 140                             |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| CCC                             | GAA | TGT | CCG | TTC | TGT | GGG | AGA | ATT | GAG | AGG | TAC | AGT | CAA | GAT | ATG | 594 |  |
| Pro                             | Glu | Cys | Pro | Phe | Cys | Gly | Arg | Ile | Glu | Arg | Tyr | Ser | Gln | Asp | Met |     |  |
| 155                             |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| GAA                             | ATT | CAT | GTG | AAA | ACA | AAG | CAT | GCC | AGC | CTT | CTA | GAA | AGT | CCG | TTA | 642 |  |
| Glu                             | Ile | His | Val | Lys | Thr | Lys | His | Ala | Ser | Leu | Leu | Glu | Ser | Pro | Leu |     |  |
| 170                             |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| GAA                             | GAC | TGT | CAT | CAA | CCA | CTC | TAT | GAC | TGT | CCC | ATG | TGT | GGG | CTT | GTC | 690 |  |
| Glu                             | Asp | Cys | His | Gln | Pro | Leu | Tyr | Asp | Cys | Pro | Met | Cys | Gly | Leu | Val |     |  |
| 185                             |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| TGT                             | ACA | AAT | TAT | CAC | ATT | CTC | CAA | GAA | CAT | GTG | GAC | TTG | CAT | TTA | GAA | 738 |  |
| Cys                             | Thr | Asn | Tyr | His | Ile | Leu | Gln | Glu | His | Val | Asp | Leu | His | Leu | Glu |     |  |
| 205                             |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| GAA                             | AGC | AGC | TTT | CAA | CAA | GTA | CTT | GTG | AGT | GGG | TAT | GTG | CCT | GTG | TGG | 786 |  |
| Glu                             | Ser | Ser | Phe | Gln | Gln | Val | Leu | Val | Ser | Gly | Tyr | Val | Pro | Val | Trp |     |  |
| 220                             |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
| ACA                             | CCC | GAC | CTG | CGA | TGT | CAT | CCT | CAG | GAA | GGC | CGT | ACA | ACT | CCT | TTA | 834 |  |
| Thr                             | Pro | Asp | Leu | Arg | Cys | His | Pro | Gln | Glu | Gly | Arg | Thr | Thr | Pro | Leu |     |  |
| 235                             |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |



|                                                                   |      |
|-------------------------------------------------------------------|------|
| AGA TGAGTTTCTT AGTATCTTGG AACACACCAG TTAAGCTCCC AAGTTTGCTT<br>Arg | 887  |
|                                                                   |      |
| CTATCTCCAC CTCCCTAATA ATGCTGGAGT TACAATCATG GACAACCATA CACACATGTT | 947  |
| TCACATGATT CTGGGCACTG AGCTTAGGTC CTTATGTCTG TGAGGCAAGC TCTTCCTGAC | 1007 |
| CGAGCTATCT CCTGAGCCTG CTGTCTGTCT CTTTAAATAA TATTAAATAC TTCATATAGA | 1067 |
| GCTCTCGAAG GTATAGGGTC TTGTATGAGT CTCCTAGGGC CACTGAAAAA TAAAGTGACC | 1127 |
| TCTAAGAGAA GTTGTTTATA TTTTATTAC TCTGTCTAGTA TTTGGGAGTA TGTAGACAGC | 1187 |
| TCCTGGTAAA GTAGGAGATT TTAGCGTTCG ATGATTTACC ACCAATAACC GTGATCTCTA | 1247 |
| TGCATCATGT ACCTGCTTTG CTCATTACCA CAAGAGGAAA ATTAGTAGAA TATTCTTTTT | 1307 |
| TTTCCTTTTC CTTTTTTTTT TTTTTTTCGG AGCTGGGGAC CGAACCAAGG GCCTTGCACT | 1367 |
| CGCTAGGCAA GCGCTCTACC ACTGAGCTAA ATCCCCAACC CCAAATTAGT AGAATATTGA | 1427 |
| TGGAAGATTA TTTCACGTCA GTGGTCTTCT GCTGTCTACC CCAGTTGGCA TGCCACTGTC | 1487 |
| GTGTTTTAGG GTTCCTGTTG CTGTAATAAA ACACTACCAA CAAGAGTAAC CTGGGCAGGA | 1547 |
| AAGGGTTTAT TTTATCCAAA CATTTCCAGT TCACCACTGA GGAATTCAG GGAAGGGACT  | 1607 |
| CAAGGCAGGA ACCTGTAGGC AGGAGCTGAT GCAAAGGCCA TGAAGTGCTG CTGAGTGGCT | 1667 |
| TGTTTTGCCC TGACTTGTTT AGACTCCTTT CTTAGAGCAC CCAGGGATAT CAGCCCAGGG | 1727 |
| GTGGCATCAC CTACAAGGAC TGGGCCTTCC AACACCAGTC ACTACAGAAC GCACTACAGA | 1787 |
| CTTGCCTGCA CTCGGTCTTT CTTTACTGTT GTATTGTTTT TTGAGATGGA GTCTCACTAT | 1847 |
| GTAGCTCTGG CTAAGTGTA ACTCTAGCTT GTGTCAAGTT GACCTAAAAC TAGCCAGCAC  | 1907 |
| AGCTATCTTC CTTTGAGTAA GATTGTAAGA GGATGCTGTG GAAGGGGTAA TTTTTTCAAA | 1967 |
| GCAGAATGTC TGATAATTCT TACTTTAGGG ATAGGCTTTG TATTGTATTC TATAAACCAA | 2027 |
| TGAAACAGTC TCAGGGCATG CTAAAAATCA GTTGTGCAGT ACATGCCCAA GAGTGGAAC  | 2087 |
| TAGAACAGT GGAAGGTGT AAAATGGGTT AATCAACAGG TGTGTGCATT GTACTGTCTC   | 2147 |
| TGAATTGAGG AGTACCTAGA AGACTCCTAA CTGTTTCTTC TGGGTGTATC TCTGAGGATG | 2207 |
| TTTTTCAGAA AACTGATGGG TGCGTTGGCA AACAGAATGA AGAAGATGTG CATTCAGCGT | 2267 |
| GGGCAAGTAG TGTCCAGTGT CGCTAGTACT ATAGGTGGAC CAGGAAAGCC GAAGCAGTGG | 2327 |
| CAGAATCACT TTGGCTCCTC CTTCTGGATG GGGCTTTCTT TCCCTGCAGC TGCTCCCTGG | 2387 |
| GTGCAGCTGC TCCCTGGGTT AACTCCAGG ATGTCTGACT TTTGGATGCT GGAACCTCTGA | 2447 |
| TAATCCCTAC CAGAAATTTT GAGCCTTTGA CCTCACACTG GGATATCTGA TTTTGCCAAA | 2507 |
| CTGGTTCTGG CACTTTCAAC TTTCACACT GGTTCCTCTG TGTCTCAGGC TATCAAGAAC  | 2567 |
| TTTTCATTTG TATCATTATG TGATCTATTC CCGTATGATT CGTGATATTT AATAAGGTTT | 2627 |
| TCTATATCTT TCTGTCTGTC TGTCTCTGTG TGTGTGTGTA CATAACACA CACGCCTGTG  | 2687 |



| 180                                                                                                                                                   | 185 | 190 |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|------|
| CAG GGG ACC AAG GCC TGG ATT GGA GCA TGT GAG ATC TAT ACA CTT CTG<br>Gln Gly Thr Lys Ala Trp Ile Gly Ala Cys Glu Ile Tyr Thr Leu Leu<br>195 200 205     |     |     | 3727 |
| ACC TCA CTG AAA GTC AAG TGC CGC ATT ATT GAT TTT CAC AAG TCA ACT<br>Thr Ser Leu Lys Val Lys Cys Arg Ile Ile Asp Phe His Lys Ser Thr<br>210 215 220 225 |     |     | 3775 |
| GGT CCT TCA GGC ACA CAC CCT CGC TTA TTC GAG TGG ATA CTG AAC TAT<br>Gly Pro Ser Gly Thr His Pro Arg Leu Phe Glu Trp Ile Leu Asn Tyr<br>230 235 240     |     |     | 3823 |
| TAT TCC TCA GAG ACG GAA GGG GCG CCA AAG GTC GTG TGT ACA TCC AAA<br>Tyr Ser Ser Glu Thr Glu Gly Ala Pro Lys Val Val Cys Thr Ser Lys<br>245 250 255     |     |     | 3871 |
| CCT CCT GTC TAT CTC CAG CAT CAG GGT CAC AGT CGA ACA GTT GTT GGG<br>Pro Pro Val Tyr Leu Gln His Gln Gly His Ser Arg Thr Val Val Gly<br>260 265 270     |     |     | 3919 |
| ATT GAA GAG AGA AAA AAC CGA ACA TTA TGT TTG CTA ATA TTT GAT CCT<br>Ile Glu Glu Arg Lys Asn Arg Thr Leu Cys Leu Leu Ile Phe Asp Pro<br>275 280 285     |     |     | 3967 |
| GGA TGT CCT TCT CGA GAA ATG CAG AAG CTG TTA AAG CAA GAC ATG GAG<br>Gly Cys Pro Ser Arg Glu Met Gln Lys Leu Lys Glu Asp Met Glu<br>290 295 300 305     |     |     | 4015 |
| GCT GGT AGT CTC AGG CAG CTC CGG AAA TGT GTG GGA AAT CTG AAG CAT<br>Ala Gly Ser Leu Arg Gln Leu Arg Lys Cys Val Gly Asn Leu Lys His<br>310 315 320     |     |     | 4063 |
| AAG CAG TAC CAG ATA GTA GCA GTG GAG GGT ATC CTG TCC CCA GAG GAG<br>Lys Gln Tyr Gln Ile Val Ala Val Glu Gly Ile Leu Ser Pro Glu Glu<br>325 330 335     |     |     | 4111 |
| AGA GCT GCC AGG AAA CAA GCT TCT CAA GTG TTT ACA GCG GAG AAG ATT<br>Arg Ala Ala Arg Lys Gln Ala Ser Gln Val Phe Thr Ala Glu Lys Ile<br>340 345 350     |     |     | 4159 |
| CCT TGACCCAGAT ATTTTGTAAT TATCCTTTTT GTTCCGATA TTGAACTCTG<br>Pro                                                                                      |     |     | 4212 |
| ATACAGTTGA AGAATTGAC TTCACTGAAG TCGGTGATAA ATTATTTAAG TTATAAATGC                                                                                      |     |     | 4272 |
| CTGTTGTACT CCTTAGCATT TCGTTGTCTG GTAATCAGTT GAATAAATTC CTTGTTTACA                                                                                     |     |     | 4332 |
| TTAAAAA                                                                                                                                               |     |     | 4339 |

## (2) INFORMATION FOR SEQ ID NO:18:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Leu Ser Cys Asp Ile Cys Gly Glu Thr Val Thr Ser Glu Pro Asp  
 1 5 10 15  
 Arg Lys Ala His Leu Ile Val His Met Glu Asn Glu Ile Ile Cys Pro  
 20 25 30  
 Phe Cys Lys Leu Ser Gly Ile Asn Tyr Asn Glu Met Cys Phe His Ile  
 35 40 45  
 Glu Thr Ala His Phe Glu Gln Thr Thr Pro Glu Lys Ser Phe Glu Thr  
 50 55 60  
 Leu Ala Ala Val Gln Tyr Glu Asn Ser Asp Leu Gly Asn Thr Lys Leu  
 65 70 75 80  
 His Ser Thr Val Glu Val Thr Ser Gly Ile His Ser Ala Cys Ala Ser  
 85 90 95  
 Asn Phe Pro Lys Glu Ser Ser Glu Ser Leu Ser Lys Asp Arg Thr Leu  
 100 105 110  
 Lys Gln Glu Ala Phe Tyr Thr Glu Ser Val Ala Glu Ser Arg Lys Tyr  
 115 120 125  
 Gln Lys Ser Arg Glu Lys Gln Ser Gly Leu Ser Glu Ala Gln Gly Ser  
 130 135 140  
 Ile Tyr Glu Thr Thr Tyr Ser Pro Pro Glu Cys Pro Phe Cys Gly Arg  
 145 150 155 160  
 Ile Glu Arg Tyr Ser Gln Asp Met Glu Ile His Val Lys Thr Lys His  
 165 170 175  
 Ala Ser Leu Leu Glu Ser Pro Leu Glu Asp Cys His Gln Pro Leu Tyr  
 180 185 190  
 Asp Cys Pro Met Cys Gly Leu Val Cys Thr Asn Tyr His Ile Leu Gln  
 195 200 205  
 Glu His Val Asp Leu His Leu Glu Glu Ser Ser Phe Gln Gln Val Leu  
 210 215 220  
 Val Ser Gly Tyr Val Pro Val Trp Thr Pro Asp Leu Arg Cys His Pro  
 225 230 235 240  
 Gln Glu Gly Arg Thr Pro Leu Arg  
 245

## (2) INFORMATION FOR SEQ ID NO:19:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Asp Arg Val Gln Cys Ser Ser Asp Arg Glu Leu Ala His Gln Leu  
 1 5 10 15

Gln Gln Glu Glu Glu Arg Lys Arg Lys Ser Glu Glu Ser Arg Gln Glu  
                   20                                  25                                  30  
 Arg Glu Glu Phe Gln Lys Leu Gln Arg Gln Tyr Gly Leu Asp Asn Ser  
                   35                                  40                                  45  
 Gly Gly Tyr Lys Gln Gln Gln Leu Arg His Met Glu Leu Glu Val Thr  
                   50                                  55                                  60  
 Arg Gly Arg Met His Pro Ser Glu Phe His Ser Arg Lys Ala Asp Met  
                   65                                  70                                  75                                  80  
 Leu Glu Ser Ile Ala Val Gly Ile Asp Asp Gly Lys Thr Lys Thr Ser  
                                   85                                  90                                  95  
 Gly Ile Ile Glu Ala Leu His Arg Tyr Tyr Gln Asn Ile Ala Thr Asp  
                                   100                                  105                                  110  
 Val Arg Cys Val Trp Leu Ser Thr Val Val Asp His Phe His Ser Ser  
                   115                                  120                                  125  
 Phe Gly Asp Lys Gly Trp Gly Cys Gly Tyr Arg Asn Phe Gln Met Leu  
                   130                                  135                                  140  
 Leu Ser Ser Leu Leu Gln Asn Glu Val Tyr Ser Asp Cys Leu Lys Gly  
                   145                                  150                                  155                                  160  
 Met Ser Val Pro Cys Ile Pro Lys Ile Gln Ser Met Ile Glu Asp Ala  
                                   165                                  170                                  175  
 Trp Asn Glu Gly Phe Asp Pro Gln Gly Ala Ser Gln Leu Asn Asn Lys  
                   180                                  185                                  190  
 Leu Gln Gly Thr Lys Ala Trp Ile Gly Ala Cys Glu Ile Tyr Thr Leu  
                   195                                  200                                  205  
 Leu Thr Ser Leu Lys Val Lys Cys Arg Ile Ile Asp Phe His Lys Ser  
                   210                                  215                                  220  
 Thr Gly Pro Ser Gly Thr His Pro Arg Leu Phe Glu Trp Ile Leu Asn  
                   225                                  230                                  235                                  240  
 Tyr Tyr Ser Ser Glu Thr Glu Gly Ala Pro Lys Val Val Cys Thr Ser  
                                   245                                  250                                  255  
 Lys Pro Pro Val Tyr Leu Gln His Gln Gly His Ser Arg Thr Val Val  
                                   260                                  265                                  270  
 Gly Ile Glu Glu Arg Lys Asn Arg Thr Leu Cys Leu Leu Ile Phe Asp  
                   275                                  280                                  285  
 Pro Gly Cys Pro Ser Arg Glu Met Gln Lys Leu Leu Lys Gln Asp Met  
                   290                                  295                                  300  
 Glu Ala Gly Ser Leu Arg Gln Leu Arg Lys Cys Val Gly Asn Leu Lys  
                   305                                  310                                  315                                  320  
 His Lys Gln Tyr Gln Ile Val Ala Val Glu Gly Ile Leu Ser Pro Glu  
                                   325                                  330                                  335  
 Glu Arg Ala Ala Arg Lys Gln Ala Ser Gln Val Phe Thr Ala Glu Lys  
                   340                                  345                                  350

Ile Pro

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2415 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: HW035
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: complement (1738..1910)
  - (D) OTHER INFORMATION: /label= SAC\_24468

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

|                                                                     |      |
|---------------------------------------------------------------------|------|
| GTTCGACGGGC CCTATTCTGC CTCCTTCAGG ATCTGCGTCT TCCAGGGATC CGCTGTTTCGA | 60   |
| CTTGGAGGTG CTTCTCTGCA GGTCCCAAGC CTGCCTCCTC ACCCCAGCTT TCCAGTGGAG   | 120  |
| GCTGCCCCCT TCCAGGCTTG GCTCAGGAAG CTCCTCATAG GCGGATGCCC ACCCATAAGA   | 180  |
| GGCTACATCC CTTTGTGGTC ACATGGCCTG TAGCCTCTTG CTGACATTGC TGGTGTCTTC   | 240  |
| TCTGGGGCCC TGGATCCCTG ACAAGCACAG AAATGTGATC TGGTAAAAGG AAAGACTGTG   | 300  |
| GCCTGATAGG CCTTTACCTC GTAGGCAGCA GGATTTTCAC TCAGTTTGAC ACAGCATGCA   | 360  |
| GTGCTCTGGG AGCAGGACCT CTGCCACCCT GGCATTTTTG GTAGGCTGGT TTGGCTCAAG   | 420  |
| GTGCTCAGAC ACTCCCATTG ATGCCTGAGT CGGATATGGG TGGAAATCTG GACTGTTGAT   | 480  |
| TATAAGTTAC CAGGTGACCT CATTCCCTCC CTTTGTCTCT TAACTGGTAT CCAGTGAGTT   | 540  |
| GCTGATGCCG ACTGGCAAGC AGAGCTGGCC CATGCCTAGA GGAGGAGAGG GACAGGCTTT   | 600  |
| CTGAGTGCTT TGATTCTGGC TGGGCTGTAG TGTATAGCTG AGAATGGCCT CCTGCATGGG   | 660  |
| TCCAGCCTTT TGGGAGGATG AGGAAGAGGA GGCTGAGGCT AGATGTGTGT TAAACAGGAG   | 720  |
| TAGCAGATCT TTGCTTCTGA ACCGGATAGA GCCGTGCTCA AGGCTTTCAG GTTTGCAGTA   | 780  |
| TCTTCTTATT GAGTCTGGGG AACGTTCCCT ATTGAGCCAG CCCTGCAGCT CCACTCCCTG   | 840  |
| CCCCATTCCC CTGATTTCTT GACAGTAAAT CCTGTGTCCA GTTGTGACTG TTGGCTGTTT   | 900  |
| TCCTGATCAT TGTTAATTCC GTTTTCCTAC TGTGAGGGTG TTGTGTTTGA CTTTCTGACA   | 960  |
| CAGCGAATGG AGAGCTTGGG CTGAGGCCAG GTCTCCCAA CTTCTCCGCT AAGTAAACCG    | 1020 |
| TAATGTGTGA CTTCCCTCCT ATCTTGACTG CCCGACTCCT TCCTTCCACA TGGACACTCA   | 1080 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GATTTCAAAG AAAACCCGCA GGAGGTGGGT CAGTTTCCTC TGTAGAATAT GGTCCCAGAG  | 1140 |
| AGTCCTCCCC TCTGTTGTGT CTAGCTGCTA GTCTGGGTGT TGTACCATCA GTGCAGGGAG  | 1200 |
| TCCACGGCAA CACTGAGTTA TACAGGGACC ACTACCATCG CCAGGCTTCC TAGCAGGCTG  | 1260 |
| TTCTCAGTTC ATCTTTCAGG TCCGTGTGTA CTCTGTGCTA GCAGCAGCCT TGGTGTTCAA  | 1320 |
| GGCCAGGATT TGCAGTTTTC ATAAGCTACA GCCCACCTGG AGATGGTGAG GCCACTTCCC  | 1380 |
| TGCTACCTCC CTCTCTGGTG TGGCCACTTG GCCAAAGCTC CCATCCACAG CTGGGGTGTC  | 1440 |
| TGAGCCACAG CCTGCTACAC TGTTTCCGCT CTGGGATCTT CTGAGTTACT CTTTTAGGCT  | 1500 |
| GTGGTTTGGT GAAAGGAACC AACACATTAA CGATCTCCCC CCCCCCCCCC AAAGCCACTG  | 1560 |
| AGTAATTCCTT GGCATGTTTT CTAAGTGCTG TTGGCTGCCT GGTTCGGGAG CAGTTGTGGA | 1620 |
| GAGGACAGAC TTAGTACCAC ACAGAGGCAT GGGTGTGCGA GCTGCTCACA GCTTCCTTGT  | 1680 |
| TTCTGGCATG TGTCCTGGGT GCGTGCTATA CCTCCCGGGC CAGCTGCACA CCTATGTACT  | 1740 |
| CTGCCCCGTA GAGGTAGAGT GTTCAGGAAG TGTCCTGAT AGATTCCCTG TTCTCTGTGG   | 1800 |
| CCCCAGTTGG GCTTTTGGCT CCTCCAGCAA CTTTCATGCC CAACCCTACC TTTCTCCCA   | 1860 |
| TTTCTCTCTG TCTGCTAGTC CCTGAAGCCT TTAACCAAAT GGAATGGGT ACAGAAAGCC   | 1920 |
| TTCTCCTGGC AACTTAGGGC AACAGGACAA GGGCTATTGT GTGTCCAAC CTGTTGGTCT   | 1980 |
| CCTGGTGCTG AGAGGTGTGT CCAAGCAGAG TTGATCAGCC CCTGCCTGCC CTGCAGGGCT  | 2040 |
| GAAGCCAGGG GGAGGTTAGT AGAGAGTACC CTAAATGGGG TGAGGGTCCT TAAACATCCA  | 2100 |
| AGTGAGGAGG GGCTGTTGTG TGGCTGCAAG GTGAGACCCT GTCTCCAGCA CCTGGGTAGG  | 2160 |
| GCCATCGGGG ATCTGGCTGC AAGGTGAGGT CTGGACTTGG CATCAGTGCA GAGCGATCAA  | 2220 |
| GTCACCTGGC CTCAGCAGGC AGCAGCCTTG GTGCCCACCC GTGCCCTGCG CAGTATTTAT  | 2280 |
| TGCTAAATTA TTGTCCAGGA GGGCGGCAC TGGGCCTGGC CCCCCGGGTA TTTATTGCTG   | 2340 |
| TACATAGTGT ATGTTTGTGA TATATAAGGT TTTCTTTATT TTGTATATGA TCAATAAACG  | 2400 |
| CCTTTTAAAG AAAAA                                                   | 2415 |

## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3531 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: HW036

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION: complement (2541..2575)  
 (D) OTHER INFORMATION: /label= SAC\_24406

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GTCGACTGAA AACCACCTCAG AATTTTCTCT GGTCTTAAC AGAAAAGAAT CAAAGTAGGA  | 60   |
| AGCACAGTAG CTGCCACATC TGTTC AACCT CTGGGCCTCC CAAGTACACC AGAGAAAACA | 120  |
| GATCAATGCT GTTCTGAAT GATTCTGCTG GTTAAAGTCA TTTATAGAAG ATTACAGATA   | 180  |
| CTGAACAACT ATGGGTAAAG AACTTACTGT GTTTTGTGAA TTGCCCAATG GAGAGAGTGT  | 240  |
| GTTCAAGGAT GACTCTTGAT CAGATTACAC AGTATGTGCA TCCAGGAGGC CACATGAAAT  | 300  |
| CAGCATAGTT AGTAACATAG AATCTGTTGT CAGCCTCCTC CAACTCGTGT CTGTTTCTTG  | 360  |
| GTTTCAATTT TAGGCCAGCC CTCTCCTCAT AAAGGGGTGA TAGTAGCCAC AGTCCACAGC  | 420  |
| CTCAAGGTCT GGTCTCCAAA AAGAAGAGTG TGAGCTGGGC CACAATCATA CCCTCCTGAA  | 480  |
| GAACTCTGGT CTTTCTGGT CATATGCTCC TGCCCCACCC TTGGTGATCC TGGCTAGATC   | 540  |
| ATGGTCTCCC GTACTGTGCC GACACCATT CACAGTAACAT AGGATGAGTT ATGGGCCTCA  | 600  |
| TCCCTAAACA CTGGAACCTG CAGCAAATGA TGTAGCAGAT ATTCACTCTA GATAACAAAT  | 660  |
| GTCAGTGACA TGAAGTGGCT AGGAAAGTTT AGAACCTGA TCATTTTATT TTTACCACTT   | 720  |
| AACACAGTAG AGAGCCATCA GGAATAATC TTTGGTGTGA TTCTTGCCAT TGAAGTCATT   | 780  |
| ATAGCTTCCA TATTGTTCG TAGTTCACTG GAAAGTGCAC TTGCTGTTAA AAGTTTGTAA   | 840  |
| GCTGTGAGGA TTCCCTAGGG TGTCAGTAA GTCTGCTCTG TATACTGCCC CCACTGGGAG   | 900  |
| TGCACGGTAC TGCACCCCTA AATCCTGCCG CCTGTGTCCC AAACATGGTG TCTGCGTGCA  | 960  |
| GTGTGGAGTA GTGCGCCTT TTTTTFMTT TTTTTFMTT CCTATTCCTT TTTTGGAGCT     | 1020 |
| GGGAACCGAA CCCAGGGCCT TGTGCTTGCT AGGCAAGTGC TCTACCACTG AGCCAAATCC  | 1080 |
| CCAACCCCTG TAGTGCGCCT TCTATACTAG AAAGCTTGAC CACTGAGCCA CACCTCCCAC  | 1140 |
| TAGTGCTTCA ATGTCAACCG AGAGTAAAT GTGTTTGTAT GAAATGCCTC CATTTGACTA   | 1200 |
| GATAGAGCTT TATTTGGAGA AAGTCACATA TAACATAATT GAACTTTGAA TTATACAATC  | 1260 |
| CCGTGGATTT TAGAGTGCTC CTGGAGCAGG TGGCAGTCAC CACTATCTAC TTCCAGAACA  | 1320 |
| GTCTCATCCT TTCCAGAAAC CCACACTCTG TCTTTCCTCT ATTCCAGATC TGTTAGACGA  | 1380 |
| GTGGAATTAC ATAGTCCGGT CTTTCTGAG TTCTGTTACT AAGTTTAAA GGTATTCT      | 1440 |
| CAGGTAGCAT CAGTCCGTAA TGTATTACTG CTGAATAGTG TTCCGTGTAT ACAGACACCG  | 1500 |
| TGTGTGCTT CTTCCAGCGA GCAGAGGAAC TCTGAGCTGT TTCTACTTTG GGGCTTTTGA   | 1560 |
| CTAATGCTAT GAACATCTGT GAAAAGTTC GAAATGTTT ATTTAGTACA GACCCTAGTG    | 1620 |
| GGGAGCTCCG GGGTCATATT ATGACAGCCT CAATTGTACT TCCTACAGTG GTTTTACCAC  | 1680 |



|            |            |            |             |             |            |      |
|------------|------------|------------|-------------|-------------|------------|------|
| CATTTCTGTC | TCTCGTGGGA | TCTAGGCTCC | AGCATCCCTC  | ACAACTTTCT  | GCCTGAGATG | 1740 |
| AAGAGGCATC | TGATTGGGAT | CTTGGTTTGC | ATTTCCCTAA  | TGTCTAATAA  | TCTGAGCTTT | 1800 |
| TTTTCATGTG | TTCATTGGCT | TTCTATGCTG | CTTTGCAGAA  | TGTTTATTTT  | AGGCTACAGT | 1860 |
| CTGCCCTTCA | GCTGGGTTAT | CTTTCTGTTT | TTCTGTAGGA  | TTTTTTATTT  | ACGGTCAACT | 1920 |
| CATCTCTTAA | AGATTAATTG | GCATTTTTTT | TTTTCTCAAC  | TTGTGGTTTG  | CCCTTCTCAA | 1980 |
| TGTCTTGATG | CTCTCTGAAG | CACAGTTTTT | ATTTTATAT   | ATTGCCTTTC  | TGCGTCTTAG | 2040 |
| CCCAGGCTGG | CCAGGAATCC | CCAAAGCCTT | GTACACAGAG  | TGAGCATTTT  | CACCGCCTCA | 2100 |
| CTTCCAGAA  | GGCACACGGC | GCTGCTCCTG | CCTAGAGCAG  | TTTTCATATT  | GGAAAATAAC | 2160 |
| AATGTGTTTT | TTCTTTCAGT | GTATCCTAAG | AAACCATTTCC | TAACCTGGAC  | TTACAGAAGC | 2220 |
| TTATGTCTTC | ACTAAAGAAT | TTTTAAATTT | TACCTCTTAC  | CTGTAGGCCT  | GTGCTCTCAA | 2280 |
| AATGTTACAC | ACCTTTATTC | ATGGCCATAT | TTAAAAATTAA | GTAGAAATAG  | TGAGTATGTA | 2340 |
| GATATGCCTG | TATCGTGATG | AGCACATTCA | CAGTGCAGTG  | CAGTTGGCCT  | GCAGCCCAGT | 2400 |
| TCTGCATCCA | CCTCAGAAAA | TGCCCAGTGA | GCCCATCTAA  | TGACTCCCAG  | CCCCTGCCAG | 2460 |
| GTCTCCCTC  | CCTGCCCTGT | CTTGGCATA  | TCTCTTCTCC  | ATGGCAATCA  | CCATTCTCTG | 2520 |
| TCCTGTTTCT | GAATTTGAGT | ACCCTAAGTG | CCTGGTATAC  | ATAGATTCTC  | AGTGCCTGTG | 2580 |
| TGTGTGTGTG | TGTGTGTGTG | TGTGCGTGCG | TGTTCATGTA  | GCAGAAATGCC | GTGAAGGCTT | 2640 |
| GTATCATGTA | TGAGTTTCTT | TTGTAAGGAC | AAATAGTACT  | TTAGACTTTA  | GTGTGTGTTG | 2700 |
| TATGTATGCT | GTATGTTTCT | TGTTACCTAC | TCATCCAGCC  | GTGGGTACCT  | CAGTTGTTCC | 2760 |
| CACCTTGAG  | CTCCTGACTA | TGCTGTGAAC | ATGTATATAC  | AAATATCCCT  | CGGATCCTGC | 2820 |
| TTAGCATACA | CGCAGCAGAT | TGTATGTCTT | AGGGTAACTC  | TGCTGTTATT  | AGTAGGCACT | 2880 |
| GCCGTAGTCT | CCATAGTGAC | CACACTATTG | TATGTCTCTG  | CAGCAGTGCA  | CAGAGATTAG | 2940 |
| AAGTGCCCAT | GTCCTTGTGA | GTCTTACTCT | TTTTTTTAGTG | GCTGTTCTAG  | TAGGTGTTAA | 3000 |
| GATCTGCTAG | TGCTTCTGCT | TCCCATCTCT | CTGACTACTG  | ATGTCACATG  | TTTTATATGC | 3060 |
| TTGGTGGCCT | TCTTTATATA | TCGTTTGAAG | AAATCTCTTT  | AGGTCCACTG  | CCCATTAATA | 3120 |
| GTGGGTCGT  | TGGCTCTGGT | TGAATTTTTG | GTAGTCACAT  | CCACAAAAGC  | ATTAACCCAC | 3180 |
| CCAAGGGAGC | CTACTACAGC | TTGCCCTAGG | AAACTTGATT  | TTAGCTCTTA  | GCTTTGCTCT | 3240 |
| CTGGTATATT | TTGAGTTCAT | TTGTGTGTGA | GATGTAAGGT  | CTGACTTTCT  | ACTCTACCCA | 3300 |
| TGTGGATACC | TGGCTTTGCA | TGTTGCCCTT | GGTGGGAAAA  | CATCCCGCTG  | TGCATGGTGG | 3360 |
| GGCTGTTTCT | GAGCCTGGTC | TCTTCCATGA | CCTCTGTCTG  | CCTTCATGCC  | AACGCCACTG | 3420 |
| CTTTGATTAC | TGGAGAATTA | TAATAGAAAT | TTGAAATCAG  | AAAATGTTTG  | TTCTGTAATA | 3480 |
| AAAATTTGAA | ATCAGAAAGT | GTTCTATAAT | AAAAATTTGA  | AATCAGAAAA  | A          | 3531 |

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2127 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: HW037

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 280..1422

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1370..1796  
 (D) OTHER INFORMATION: /label= SAC\_24354

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GTCGACCTGC GGCTGGCCGG CGGGGCAGGC CCCGGACCCG TCGGGTTCCT GGGCATGGTG | 60  |
| AGCAAGGGGC TGCTGCGCCT TGTCTCTTCA GTCAACCGCA GGAAGATGAA GCTTCTGCTG | 120 |
| GGCATCGCGC TGTTGCGCTA CGCCGCCTAA CTTGCTCATG ATGGAGTGCC AAGTGCCTCA | 180 |
| GAGAAACAGG CCACCAGAAG AACAGTGCAT TCTCAGTACA AGGGCAGCGT TCAGCATTTG | 240 |
| GATATTGGAG TTGAAGCTGT TTGGGGCAAC TTTGTTAAC ATG AGG TCT ATC CAG    | 294 |
| Met Arg Ser Ile Gln                                               |     |
| 1 5                                                               |     |
| GAA AAT GGT GAA CTA AAG ATT GAA AGC AAG ATT GAA GAG ATT ATT GAA   | 342 |
| Glu Asn Gly Glu Leu Lys Ile Glu Ser Lys Ile Glu Glu Ile Ile Glu   |     |
| 10 15 20                                                          |     |
| CCA TTA AGA GAG AAA ATC AGA GAT TTG GAA AAA AGT TTC ACC CAG AAA   | 390 |
| Pro Leu Arg Glu Lys Ile Arg Asp Leu Glu Lys Ser Phe Thr Gln Lys   |     |
| 25 30 35                                                          |     |
| TAC CCA CCA GTA AAG TTT TTG TCA GAA AAG GAC CGG AAG AGG ATT TTG   | 438 |
| Tyr Pro Pro Val Lys Phe Leu Ser Glu Lys Asp Arg Lys Arg Ile Leu   |     |
| 40 45 50                                                          |     |
| ATC ACT GGA GGT GCG GGC TTT GTG GGC TCC CAT CTA ACT GAC AAA CTC   | 486 |
| Ile Thr Gly Gly Ala Gly Phe Val Gly Ser His Leu Thr Asp Lys Leu   |     |
| 55 60 65                                                          |     |
| ATG ATG GAT GGC CAT GAG GTG ACC GTG GTG GAC AAC TTC TTC ACA GGC   | 534 |
| Met Met Asp Gly His Glu Val Thr Val Val Asp Asn Phe Phe Thr Gly   |     |
| 70 75 80 85                                                       |     |
| AGG AAG AGA AAT GTG GAA CAC TGG ATT GGC CAT GAG AAC TTC GAG CTG   | 582 |
| Arg Lys Arg Asn Val Glu His Trp Ile Gly His Glu Asn Phe Glu Leu   |     |
| 90 95 100                                                         |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| ATT AAC CAT GAT GTG GTA GAG CCA CTC TAC ATC GAA GTT GAC CAG ATC<br>Ile Asn His Asp Val Val Glu Pro Leu Tyr Ile Glu Val Asp Gln Ile<br>105 110 115     | 630  |
| TAC CAT CTG GCT TCT CCA GCC TCC CCT CCA AAC TAC ATG TAC AAC CCC<br>Tyr His Leu Ala Ser Pro Ala Ser Pro Pro Asn Tyr Met Tyr Asn Pro<br>120 125 130     | 678  |
| ATC AAG ACC CTG AAG ACA AAT ACA ATT GGA ACA CTA AAC ATG TTG GGA<br>Ile Lys Thr Leu Lys Thr Asn Thr Ile Gly Thr Leu Asn Met Leu Gly<br>135 140 145     | 726  |
| CTG GCA AAG CGT GTG GGT GCC CGT CTG CTC CTA GCC TCC ACA TCT GAG<br>Leu Ala Lys Arg Val Gly Ala Arg Leu Leu Leu Ala Ser Thr Ser Glu<br>150 155 160 165 | 774  |
| GTA TAT GGA GAT CCT GAG GTC CAC CCT CAA AGT GAG GAC TAC TGG GGC<br>Val Tyr Gly Asp Pro Glu Val His Pro Gln Ser Glu Asp Tyr Trp Gly<br>170 175 180     | 822  |
| CAC GTG AAT CCC ATA GGA CCC CGA GCC TGC TAT GAC GAG GGC AAA CGT<br>His Val Asn Pro Ile Gly Pro Arg Ala Cys Tyr Asp Glu Gly Lys Arg<br>185 190 195     | 870  |
| GTT GCG GAA ACC ATG TGC TAT GCC TAC ATG AAG CAG GAA GGT GTG GAG<br>Val Ala Glu Thr Met Cys Tyr Ala Tyr Met Lys Gln Glu Gly Val Glu<br>200 205 210     | 918  |
| GTG CGG GTG GCC AGG ATC TTC AAC ACC TTT GGG CCA CGA ATG CAC ATG<br>Val Arg Val Ala Arg Ile Phe Asn Thr Phe Gly Pro Arg Met His Met<br>215 220 225     | 966  |
| AAT GAT GGG AGG GTG GTC AGC AAC TTC ATC TTA CAA GCG CTA CAA GGG<br>Asn Asp Gly Arg Val Val Ser Asn Phe Ile Leu Gln Ala Leu Gln Gly<br>230 235 240 245 | 1014 |
| GAG CCG CTC ACA GTA TAT GGA TCT GGG TCT CAG ACA CGG GCA TTC CAG<br>Glu Pro Leu Thr Val Tyr Gly Ser Gly Ser Gln Thr Arg Ala Phe Gln<br>250 255 260     | 1062 |
| TAT GTT AGC GAT CTA GTG AAT GGC CTG GTA GCA CTG ATG AAC AGC AAT<br>Tyr Val Ser Asp Leu Val Asn Gly Leu Val Ala Leu Met Asn Ser Asn<br>265 270 275     | 1110 |
| GTC AGC AGC CCT GTC AAC CTG GGA AAT CCA GAA GAA CAC ACA ATC CTG<br>Val Ser Ser Pro Val Asn Leu Gly Asn Pro Glu Glu His Thr Ile Leu<br>280 285 290     | 1158 |
| GAA TTT GCT CAG TTA ATT AAA AAC CTT GTT GGT AGT GGA AGT GAA ATT<br>Glu Phe Ala Gln Leu Ile Lys Asn Leu Val Gly Ser Gly Ser Glu Ile<br>295 300 305     | 1206 |
| CAG TTT CTC TCT GAA GCT CAG GAT GAT CCA CAG AAA AGA AAA CCA GAC<br>Gln Phe Leu Ser Glu Ala Gln Asp Asp Pro Gln Lys Arg Lys Pro Asp<br>310 315 320 325 | 1254 |
| ATC AAA AAA GCA AAA CTG ATG CTG GGG TGG GAG CCT GTG GTT CCA TTG<br>Ile Lys Lys Ala Lys Leu Met Leu Gly Trp Glu Pro Val Val Pro Leu<br>330 335 340     | 1302 |
| GAG GAA GGA TTG AAC AAA GCC ATC CAC TAT TTC CGG AAG GAA CTA GAG<br>Glu Glu Gly Leu Asn Lys Ala Ile His Tyr Phe Arg Lys Glu Leu Glu<br>350 355 360     | 1350 |

|                                 |     |     |             |     |     |             |            |     |             |     |            |            |     |     |             |      |      |
|---------------------------------|-----|-----|-------------|-----|-----|-------------|------------|-----|-------------|-----|------------|------------|-----|-----|-------------|------|------|
| 345                             |     |     |             |     |     |             | 350        |     |             |     | 355        |            |     |     |             |      |      |
| TAC                             | CAG | GCT | AAT         | AAC | CAG | TAC         | ATC        | CCT | AAA         | CCC | AAG        | CCT        | GCC | AGA | GTG         | 1398 |      |
| Tyr                             | Gln | Ala | Asn         | Asn | Gln | Tyr         | Ile        | Pro | Lys         | Pro | Lys        | Pro        | Ala | Arg | Val         |      |      |
| 360                             |     |     |             |     |     | 365         |            |     |             |     |            | 370        |     |     |             |      |      |
| AAG AAG GGC CGG ACG CGC CAC AGC |     |     |             |     |     |             | TGAGTTAGCC |     | TTGGGATGCG  |     | AGACTCTATT |            |     |     | 1452        |      |      |
| Lys Lys Gly Arg Thr Arg His Ser |     |     |             |     |     |             |            |     |             |     |            |            |     |     |             |      |      |
| 375                             |     |     |             |     |     | 380         |            |     |             |     |            |            |     |     |             |      |      |
| TTACTTTATA                      |     |     | AGGTGGACTT  |     |     | TTGTGGGATT  |            |     | TTTTTTTTTTT |     |            | TTTTAAGACT |     |     | TAAACAGGTG  |      | 1512 |
| TCATGAAGAA                      |     |     | CAAACCTGGAA |     |     | TTTTATTCTG  |            |     | AAGCTTGCTT  |     |            | TAAAGACACT |     |     | GATGTGCCTA  |      | 1572 |
| AAAGCTCCCT                      |     |     | TGAACCTCTGC |     |     | AGACTTTGCC  |            |     | TTGCACTTTT  |     |            | TAACTCTGTC |     |     | TTTTTTTATGC |      | 1632 |
| ACAACAGCCT                      |     |     | AGATGCATTCT |     |     | TCTGCTATTT  |            |     | TCAGGTTTTT  |     |            | TTATCTTGCT |     |     | GTTAGAGTGT  |      | 1692 |
| ATGCTGTAAC                      |     |     | TGTCAC TGAC |     |     | AGTTTTATTT  |            |     | ACTGGTTTCT  |     |            | TTGTGAAGCT |     |     | GAAAAGAAAC  |      | 1752 |
| ATTAAATGGG                      |     |     | GTGGAAAATG  |     |     | CCAATTTTAT  |            |     | TTATAAAAGT  |     |            | GAGTACTTTA |     |     | TAAATGAGAT  |      | 1812 |
| GTTACACTAT                      |     |     | GCATAAAGAA  |     |     | TACAAACCTA  |            |     | GAGGTATGGC  |     |            | CAGCTGGGCA |     |     | GTGCACCAGT  |      | 1872 |
| GTTTATTTGG                      |     |     | GGACAGATGA  |     |     | AAGAACTCCA  |            |     | TTGGAAAGCT  |     |            | TTGCATTTCT |     |     | TTTTTTAATTC |      | 1932 |
| TGAATTTTCT                      |     |     | GAAGGTCTAG  |     |     | TTTTTCAGTTA |            |     | CAGACTTGAC  |     |            | TTTGAAACAT |     |     | CCCTGTTGGT  |      | 1992 |
| TCTTGATCAA                      |     |     | AGATATTTGA  |     |     | AATCACTACT  |            |     | GTGTTGTGCT  |     |            | GCATATTGGG |     |     | GTGGGGGTGG  |      | 2052 |
| GGACAATGTT                      |     |     | AACATATTCT  |     |     | TGGTTAACCA  |            |     | TGGTTAAATA  |     |            | TGCTATTTTA |     |     | ATAAAATATT  |      | 2112 |
| GAAACTCGTC                      |     |     | AAAAA       |     |     |             |            |     |             |     |            |            |     |     |             |      | 2127 |

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Ser | Ile | Gln | Glu | Asn | Gly | Glu | Leu | Lys | Ile | Glu | Ser | Lys | Ile |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Glu | Glu | Ile | Ile | Glu | Pro | Leu | Arg | Glu | Lys | Ile | Arg | Asp | Leu | Glu | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ser | Phe | Thr | Gln | Lys | Tyr | Pro | Pro | Val | Lys | Phe | Leu | Ser | Glu | Lys | Asp |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Arg | Lys | Arg | Ile | Leu | Ile | Thr | Gly | Gly | Ala | Gly | Phe | Val | Gly | Ser | His |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Thr | Asp | Lys | Leu | Met | Met | Asp | Gly | His | Glu | Val | Thr | Val | Val | Asp |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Asn | Phe | Phe | Thr | Gly | Arg | Lys | Arg | Asn | Val | Glu | His | Trp | Ile | Gly | His |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Glu        | Asn        | Phe        | Glu<br>100 | Leu        | Ile        | Asn        | His        | Asp<br>105 | Val        | Val        | Glu        | Pro        | Leu<br>110 | Tyr        | Ile        |
| Glu        | Val        | Asp<br>115 | Gln        | Ile        | Tyr        | His        | Leu<br>120 | Ala        | Ser        | Pro        | Ala        | Ser<br>125 | Pro        | Pro        | Asn        |
| Tyr        | Met<br>130 | Tyr        | Asn        | Pro        | Ile        | Lys<br>135 | Thr        | Leu        | Lys        | Thr        | Asn<br>140 | Thr        | Ile        | Gly        | Thr        |
| Leu<br>145 | Asn        | Met        | Leu        | Gly        | Leu<br>150 | Ala        | Lys        | Arg        | Val        | Gly<br>155 | Ala        | Arg        | Leu        | Leu        | Leu<br>160 |
| Ala        | Ser        | Thr        | Ser        | Glu<br>165 | Val        | Tyr        | Gly        | Asp<br>170 | Pro        | Glu        | Val        | His        | Pro        | Gln<br>175 | Ser        |
| Glu        | Asp        | Tyr        | Trp<br>180 | Gly        | His        | Val        | Asn        | Pro<br>185 | Ile        | Gly        | Pro        | Arg        | Ala<br>190 | Cys        | Tyr        |
| Asp        | Glu        | Gly<br>195 | Lys        | Arg        | Val        | Ala        | Glu<br>200 | Thr        | Met        | Cys        | Tyr        | Ala<br>205 | Tyr        | Met        | Lys        |
| Gln        | Glu        | Gly<br>210 | Val        | Glu        | Val        | Arg<br>215 | Val        | Ala        | Arg        | Ile        | Phe<br>220 | Asn        | Thr        | Phe        | Gly        |
| Pro<br>225 | Arg        | Met        | His        | Met        | Asn<br>230 | Asp        | Gly        | Arg        | Val        | Val<br>235 | Ser        | Asn        | Phe        | Ile        | Leu<br>240 |
| Gln        | Ala        | Leu        | Gln        | Gly<br>245 | Glu        | Pro        | Leu        | Thr        | Val<br>250 | Tyr        | Gly        | Ser        | Gly        | Ser<br>255 | Gln        |
| Thr        | Arg        | Ala        | Phe<br>260 | Gln        | Tyr        | Val        | Ser        | Asp<br>265 | Leu        | Val        | Asn        | Gly        | Leu<br>270 | Val        | Ala        |
| Leu        | Met        | Asn<br>275 | Ser        | Asn        | Val        | Ser        | Ser<br>280 | Pro        | Val        | Asn        | Leu        | Gly<br>285 | Asn        | Pro        | Glu        |
| Glu        | His<br>290 | Thr        | Ile        | Leu        | Glu        | Phe<br>295 | Ala        | Gln        | Leu        | Ile        | Lys<br>300 | Asn        | Leu        | Val        | Gly        |
| Ser<br>305 | Gly        | Ser        | Glu        | Ile        | Gln<br>310 | Phe        | Leu        | Ser        | Glu        | Ala<br>315 | Gln        | Asp        | Asp        | Pro        | Gln<br>320 |
| Lys        | Arg        | Lys        | Pro        | Asp<br>325 | Ile        | Lys        | Lys        | Ala        | Lys<br>330 | Leu        | Met        | Leu        | Gly        | Trp<br>335 | Glu        |
| Pro        | Val        | Val        | Pro<br>340 | Leu        | Glu        | Glu        | Gly        | Leu        | Asn<br>345 | Lys        | Ala        | Ile        | His<br>350 | Tyr        | Phe        |
| Arg        | Lys        | Glu<br>355 | Leu        | Glu        | Tyr        | Gln        | Ala<br>360 | Asn        | Asn        | Gln        | Tyr        | Ile<br>365 | Pro        | Lys        | Pro        |
| Lys        | Pro<br>370 | Ala        | Arg        | Val        | Lys        | Lys<br>375 | Gly        | Arg        | Thr        | Arg        | His<br>380 | Ser        |            |            |            |

(2) INFORMATION FOR SEO ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1785 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:  
(B) CLONE: HW038
- (ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1440..1714  
(D) OTHER INFORMATION: /label= SAC\_24332

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GTCGACGGTT GAGTCTGATG AGGAAGATCA AGAAAAGACT GAGGAGACTC CTTCCCAGCT  | 60   |
| GGACCAGGAT ACTCAAGTAC AGGACATGGA TGAGGGTTCA GACGATGAAG AAGAAGGACA  | 120  |
| GAAAGTGCCT CCACCCCCAG AGACACCCAT GCCTCCACCT CTGCCCCCAA CACCAGACCA  | 180  |
| AGTCATTGTG CGAAAGGACT ATGATCCCAA AGCTTCCAAG CCCCTTCCTC CAGCTCCTGC  | 240  |
| TCCTGATGAG TATCTTGTGT CCCCCATAAC TGGGGAGAAG ATTCTTGCCA GCAAAATGCA  | 300  |
| AGAACACATG CGCATCGGGC TTCTTGACCC CCGCTGGCTG GAGCAACGGG ATCGCTCCAT  | 360  |
| CCGAGAGAAG CAGAGCANTG ATGAGGTGTA CGCACCAGGT CTGGATATTG AGAGCAGCCT  | 420  |
| AAAGCAGTTG GCTGAGCGAC GTACTGACAT CTTTGGGGTA GAAGAGACAG CCATTGGTAA  | 480  |
| GAAGATTGGT GAAGAGGAGA TCCAGAAGCC AGAGGAAAAG GTGACTTGGG ATGGCCATTC  | 540  |
| AGGCAGCATG GCGCGACCC AGCAGGCTGC CCAGGCCAAC ATCACCTCCA GGAGCAGATT   | 600  |
| GAGGCCATCC ATAAGGCCAA GGGCCTGGTG CCAGAAGATG ACACCAAAGA GAAGATTGGC  | 660  |
| CCTAGCAAGC CCAATGAAAT CCCTCAGCAG CCACCGCTCC ATCTTCAGCC ACCAATATCC  | 720  |
| CCAGCTCAGC GCGCCCCATC ACGTCATTCC CCGGCCACCT GCGATGCCAC CTCCAGTCCG  | 780  |
| CACCACTGTC GTATCTGCAG TGCTGTTCAT GCCTCGGCCC CCCATGGCAT CTGTGGTCCG  | 840  |
| GCTGCCCCCA GGCTCAGTGA TTGCCCCGAT GCCACCCATC ATCCACGCAC CTAGGATCAA  | 900  |
| CGTGGTACCC ATGCCTCCTG CAGCACCNC C CATCATGGCA CCGGCGCCAC CTCCCATGAT | 960  |
| TGTGCCAACA GCCTTTGTGC CTGCTCCCCC CTGTGGCTCC AGTGCCAGCC CCAGCTCCAA  | 1020 |
| TGCCTCCCGT ACACCCCCCA CCTCCTATGG AAGATGAGCC TCCATCCAAG AACTAAAGA   | 1080 |
| CCGAGGACAG CCTCATGCCT GAGGAAGAGT TCCTGCGCAG GAACAAGGGT CCAGTATCCA  | 1140 |
| TCAAGGTGCA GGTACCCAAC ATGCAGGATA AGACAGAATG GAAGCTGAAT GGGCAGGGGC  | 1200 |
| TGGTCTTCAC TCTCCCGCTC ACAGACCAGG TCTCTGTCAT CAAAGTGAAG ATTCATGAAG  | 1260 |
| CNACGGGCAT GCCTGCAGGG AAGCAGAAAC TACAGTATGA AGGCATCTTC ATCAAGGACT  | 1320 |
| CCAACTCCCT GGCTTACTAC AACATGGCCA GTGGTGCTGT CATCCACTTG GCCCTCAAGG  | 1380 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| AAAGAGGCGG CCGGAAGAAG TAGCCTCGAG AGATACTGCA AGTGGACTCC TGCCATTGTA  | 1440 |
| CCTCTTTCCA CCACCAATTC CGGGAGTTTC CCTGGGACCT CGGGCACAGC CTGGGCATTT  | 1500 |
| GTCTCCCTCT AAGGCAGTCT ATGGAATGGA TATCTGTTTA GATTTGGATT GGAGGTCCTT  | 1560 |
| CAAGGAAGCC CATTAGGAAT TGAAAACCCA GGGTTCTCCC ACAGGAGAGC TTCATAATAC  | 1620 |
| CAAGTAATGT TTGGCTAATA GAGTATGGTT ACTACCATT C ATCATTGTGT ATCATGCTTT | 1680 |
| GGCCTCTAAT AAACCTCTTG AAGCCAGGCA TGGTACACAC ATGCCTGTAA TCCC GGGACT | 1740 |
| TGGGGGCGG GCAGAAGAAT TAAATGTTCA TCTTGGCTGT AAAAA                   | 1785 |

## (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1054 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: HW039
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 231..617
  - (D) OTHER INFORMATION: /label= SAC\_24045

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TTTTTCAGAA TTGGCTGACT TTAATTTGGA AACAGCTTTT GGCTACAGAC ATTCAGGTTT  | 60  |
| AAGGCACATT CCAAACTACA AGGATCCCTG CCACTGGCAC GGGGCCCTGGC TTAAATTCTT | 120 |
| GCATGGTTTT ACATGGAAAG TGGAACAAAT GATTTTCTGG CCTCTTCTAA AAAAGAGTGT  | 180 |
| GAGTTTGGCA AAAACAAAAC TCATGACACA TTCTCACCAG ACACCACAGT ACCGTTACAA  | 240 |
| GACCTCCCTT TTGTCCTAGG CAAAGACGGG TGGCCCGCTC ACCTACCATT CTCTCCAGAA  | 300 |
| ACATGTATAC AGTAAGCATG CTGTGTATGCG TCTGTCTGGC AGCGATGGTT AAAAAAAGTT | 360 |
| TTCAAATAAA AATACAAAAA TCACACGTCT ATAACAAAGC TAAGAGTCTT AGCCACAAGC  | 420 |
| AGCGAGGAAT GAGTGTAGGA ACCAGGAGAG ATAAACATCA ATTCTGCACA GCAAGGGGCT  | 480 |
| GTGAGGGCCA GGGAGATGGT CACCTGAGAA CCTGGCCCAC CTGGGCCCTT CGGCACAATA  | 540 |
| CGTGGATGAG GGGGGACCAG AAGGAAAAGG TCATGGCTTT GGGGATGGGT GGATGGCTGG  | 600 |
| GGGGTGCACT TGTGGGTACT AGATAGATTG GGGGAACTGG TGTGCTCTTC GGGACGTTTC  | 660 |

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CTGGCCACTG CCAGCAGGGG GCCAGCAGGG GGCACAGGTG AGCCACTGCC ACCGCTCAGT 720
CGTTGCCACC ACAGATCTTC AGCAGGATCT TCCGATAATC CCCAGAAGTG TCTCCCGTGA 780
TATCGTGGTA CAGTGACTTG CCGTACATCC GCTTATACTC TGCTCGGATA TCCAGCAGGT 840
CAAGCTCGCT TCGAGACACC ATGATGCGAA TCAGGGTCCG GTCTTTTGTG CCTGCTCCCC 900
CTCATAGCCT TGTGAGCCT TTCGGCAAAG AAGGCAGGGG TGTTCTTGAG GCATTTTACC 960
ACAGCCAGCA TGCCCTGCTC CAGGTCCCCA GACATCTCCG GCAGATGCTC TTCTCGATGT 1020
CTCGGCCTGT CATCCTCTGA TACTCGTTGA AACT 1054

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## (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3306 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW040

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 481..2433

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: complement (2395..2588)
- (D) OTHER INFORMATION: /label= SAC\_24520

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

GTCGACGCCT GGTGTGGCTG GCGGCACCAG CTGAGTATTC CCTGAAAGAA TGAAGATGAC 60
TGGCCTAGAG GAGTCAGGAA TGTGACTGCT GGGAGATCCA GCTAGAGCAA CCATACCTGC 120
TTTTCCAGGA CCTTCCCCCT AACAGCTAAG GAGCCTTAGG TCTGGGAGAG GCAGGCACCT 180
GGCTGCAGAA GGGGAAACAA CCTTTTCTC TTTCTCTCCT CCACTACTCT CCTGATGGCT 240
GCAGAAGAAG AAAGATCTAC CACGGGAAAC TCGGAGAGCT AGTCGGTTAA CTGAGCTGTT 300
GGATCTCCAC GGCACGAGGC AAATCCGTGA TGTGACTTTT TGTTTTTTCT CCTAGGTCAG 360
CTGAGGGAAC AGCTCAGTTA CCTTAAGGGC GATAACTTTT TCAGGTTTAC TTGTGCCGAT 420
TGCTCGGCAG ACGGCAAGGA GCAGTCCGAG AGGCTGAAGC TGACATGGCA GCAAGTGGTC 480
ATG CTG GCT ATG TAC AAC TTG TCT CTG GAA GGA AGT GGA CGT CAA GGC 528
Met Leu Ala Met Tyr Asn Leu Ser Leu Glu Gly Ser Gly Arg Gln Gly
 1 5 10 15
TAC TTC CGG TGG AAA GAA GAT ATC TGT GCT TTT ATT GAG AAA CAT TGG 576

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Tyr | Phe | Arg | Trp | Lys | Glu | Asp | Ile | Cys | Ala | Phe | Ile | Glu | Lys | His | Trp |      |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |      |
| ACT | TTT | TTA | CTA | GGA | AAT | AGG | AAA | AAG | ACT | TCG | ACG | TGG | TGG | AGC | ACA | 624  |
| Thr | Phe | Leu | Leu | Gly | Asn | Arg | Lys | Lys | Thr | Ser | Thr | Trp | Trp | Ser | Thr |      |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |      |
| GTA | GCA | GGT | TGC | CTC | AGC | GTG | GGA | AGT | CCT | GTT | TAT | TTC | CGT | TCA | GGT | 672  |
| Val | Ala | Gly | Cys | Leu | Ser | Val | Gly | Ser | Pro | Val | Tyr | Phe | Arg | Ser | Gly |      |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |      |
| GCT | CAG | GAA | TTT | GGA | GAG | CCT | GGA | TGG | TGG | AAA | CTT | GTT | CAT | AAC | AGA | 720  |
| Ala | Gln | Glu | Phe | Gly | Glu | Pro | Gly | Trp | Trp | Lys | Leu | Val | His | Asn | Arg |      |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |      |
| CCC | CCA | ACA | ATG | AGA | CCA | GAG | GGA | GAG | AAG | CTG | TCT | GCC | TCC | ACT | TTG | 768  |
| Pro | Pro | Thr | Met | Arg | Pro | Glu | Gly | Glu | Lys | Leu | Ser | Ala | Ser | Thr | Leu |      |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |      |
| AAA | GTG | AAA | GCT | TCA | AAA | CCA | ACA | CTG | GAT | CCC | ATC | ATT | ACC | GTT | GAA | 816  |
| Lys | Val | Lys | Ala | Ser | Lys | Pro | Thr | Leu | Asp | Pro | Ile | Ile | Thr | Val | Glu |      |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |      |
| GGA | CTC | AGA | AAA | CGA | GCA | AGC | CGG | AAT | CCT | GTG | GAA | TCA | GCC | ATG | GAA | 864  |
| Gly | Leu | Arg | Lys | Arg | Ala | Ser | Arg | Asn | Pro | Val | Glu | Ser | Ala | Met | Glu |      |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |      |
| TTG | AAA | GAG | AAG | CGG | TCT | CGA | ACA | CAG | GAA | GCT | AAA | GAC | ATC | AGA | AGA | 912  |
| Leu | Lys | Glu | Lys | Arg | Ser | Arg | Thr | Gln | Glu | Ala | Lys | Asp | Ile | Arg | Arg |      |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |      |
| GCA | CAG | AAA | GAA | GCA | GCC | GGC | CTC | CTT | GAC | AGA | AGC | ACC | TCT | TCT | ACC | 960  |
| Ala | Gln | Lys | Glu | Ala | Ala | Gly | Leu | Leu | Asp | Arg | Ser | Thr | Ser | Ser | Thr |      |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |      |
| CCT | GTC | AAG | TTC | ATA | AGC | CGA | GGC | CGG | AGG | CCG | GAT | ATG | ATT | TTG | GAG | 1008 |
| Pro | Val | Lys | Phe | Ile | Ser | Arg | Gly | Arg | Arg | Pro | Asp | Met | Ile | Leu | Glu |      |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |      |
| AAA | GGA | GAA | GTG | ATT | GAC | TTT | TCA | TCC | CTG | AGC | TCC | TCG | GAC | CGT | ACC | 1056 |
| Lys | Gly | Glu | Val | Ile | Asp | Phe | Ser | Ser | Leu | Ser | Ser | Ser | Asp | Arg | Thr |      |
|     |     | 180 |     |     |     |     |     | 185 |     |     |     |     | 190 |     |     |      |
| CCC | CTC | ACA | AGC | CCC | TCT | CCT | TCT | CCC | TCT | CTG | GAT | TTC | TCT | GCC | CCA | 1104 |
| Pro | Leu | Thr | Ser | Pro | Ser | Pro | Ser | Pro | Ser | Leu | Asp | Phe | Ser | Ala | Pro |      |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |      |
| GGG | ACA | CCA | GCG | TCA | CAT | TCT | GCC | ACG | CCT | AGC | TTG | CTC | TCT | GAA | GCA | 1152 |
| Gly | Thr | Pro | Ala | Ser | His | Ser | Ala | Thr | Pro | Ser | Leu | Leu | Ser | Glu | Ala |      |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |      |
| GAC | CTC | ATC | CCA | GAC | GTG | ATG | CCA | CCC | CAA | GCT | CTA | TTT | CAT | GAT | GAT | 1200 |
| Asp | Leu | Ile | Pro | Asp | Val | Met | Pro | Pro | Gln | Ala | Leu | Phe | His | Asp | Asp |      |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |      |
| GAT | GAG | CTG | GAA | GGA | GAT | GGA | GTC | ATA | GAC | CCA | GGG | ATG | GAG | TAC | ATC | 1248 |
| Asp | Glu | Leu | Glu | Gly | Asp | Gly | Val | Ile | Asp | Pro | Gly | Met | Glu | Tyr | Ile |      |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |      |
| CCA | CCC | CCA | GCT | GGG | TCA | GCT | TCT | GGG | CTG | ATG | GGG | AGC | AGA | AAG | AAG | 1296 |
| Pro | Pro | Pro | Ala | Gly | Ser | Ala | Ser | Gly | Leu | Met | Gly | Ser | Arg | Lys | Lys |      |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |      |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| GTC<br>Val | AGA<br>Arg | GCT<br>Ala | GCA<br>Ala | GAG<br>Glu | CAG<br>Gln | ATA<br>Ile | AAA<br>Lys | CAG<br>Gln | GAA<br>Glu | GTC<br>Val | GAC<br>Asp | AGC<br>Ser | GAG<br>Glu | GAG<br>Glu | GAG<br>Glu | 1344 |
|            |            | 275        |            |            |            |            | 280        |            |            |            |            | 285        |            |            |            |      |
| AAG<br>Lys | CCA<br>Pro | GAC<br>Asp | AGG<br>Arg | ATG<br>Met | GAT<br>Asp | GGA<br>Gly | GAT<br>Asp | AGC<br>Ser | GAA<br>Glu | GAC<br>Asp | ACA<br>Thr | GAT<br>Asp | TCA<br>Ser | AAC<br>Asn | ACT<br>Thr | 1392 |
|            | 290        |            |            |            |            | 295        |            |            |            |            | 300        |            |            |            |            |      |
| TCT<br>Ser | TTG<br>Leu | CAC<br>His | ACT<br>Thr | AGA<br>Arg | GCT<br>Ala | CGA<br>Arg | GAA<br>Glu | AAG<br>Lys | AGG<br>Arg | AAG<br>Lys | CCA<br>Pro | CCC<br>Pro | CTG<br>Leu | GAG<br>Glu | AAG<br>Lys | 1440 |
|            | 305        |            |            |            | 310        |            |            |            |            | 315        |            |            |            |            | 320        |      |
| GAC<br>Asp | ACG<br>Thr | AAG<br>Lys | CCC<br>Pro | AAG<br>Lys | GGG<br>Gly | CCC<br>Pro | AGG<br>Arg | TAT<br>Tyr | ACG<br>Thr | CCT<br>Pro | GTG<br>Val | AGC<br>Ser | ATC<br>Ile | TAT<br>Tyr | GAG<br>Glu | 1488 |
|            |            |            |            | 325        |            |            |            |            | 330        |            |            |            |            | 335        |            |      |
| GAG<br>Glu | AAG<br>Lys | CTG<br>Leu | CTG<br>Leu | CTC<br>Leu | AAG<br>Lys | AGG<br>Arg | CTG<br>Leu | GAG<br>Glu | GCA<br>Ala | TGC<br>Cys | CCT<br>Pro | GGT<br>Gly | GCC<br>Ala | GTG<br>Val | GCC<br>Ala | 1536 |
|            |            |            | 340        |            |            |            |            | 345        |            |            |            |            | 350        |            |            |      |
| ATG<br>Met | ACT<br>Thr | CCA<br>Pro | GAA<br>Glu | GCC<br>Ala | CGG<br>Arg | AGG<br>Arg | CTG<br>Leu | AAA<br>Lys | CGG<br>Arg | AAG<br>Lys | CTG<br>Leu | ATC<br>Ile | GTC<br>Val | CGG<br>Arg | CAA<br>Gln | 1584 |
|            |            | 355        |            |            |            |            | 360        |            |            |            |            | 365        |            |            |            |      |
| GCA<br>Ala | AAA<br>Lys | AGG<br>Arg | GAT<br>Asp | CGG<br>Arg | GGC<br>Gly | TTA<br>Leu | CCA<br>Pro | CTG<br>Leu | TTT<br>Phe | GAC<br>Asp | TTG<br>Leu | GAC<br>Asp | GAG<br>Glu | GTT<br>Val | GTG<br>Val | 1632 |
|            | 370        |            |            |            | 375        |            |            |            |            |            | 380        |            |            |            |            |      |
| AAC<br>Asn | GCA<br>Ala | GCA<br>Ala | CTT<br>Leu | CTG<br>Leu | TTA<br>Leu | GTG<br>Val | GAT<br>Asp | GGG<br>Gly | ATT<br>Ile | TAT<br>Tyr | GGA<br>Gly | GCC<br>Ala | AAA<br>Lys | GAT<br>Asp | GGA<br>Gly | 1680 |
|            | 385        |            |            |            | 390        |            |            |            |            | 395        |            |            |            |            | 400        |      |
| GGA<br>Gly | GCT<br>Ala | TCC<br>Ser | CGG<br>Arg | CTT<br>Leu | CCA<br>Pro | GCT<br>Ala | GGA<br>Gly | CAA<br>Gln | GCT<br>Ala | ACA<br>Thr | TAC<br>Tyr | CGG<br>Arg | ACC<br>Thr | ACC<br>Thr | TGC<br>Cys | 1728 |
|            |            |            |            | 405        |            |            |            | 410        |            |            |            |            | 415        |            |            |      |
| CAG<br>Gln | GAC<br>Asp | TTC<br>Phe | AGG<br>Arg | ATC<br>Ile | CTT<br>Leu | GAC<br>Asp | CGG<br>Arg | TAC<br>Tyr | CAG<br>Gln | ACT<br>Thr | GCC<br>Ala | TTA<br>Leu | CCA<br>Pro | GCC<br>Ala | AGG<br>Arg | 1776 |
|            |            | 420        |            |            |            |            |            | 425        |            |            |            | 430        |            |            |            |      |
| AAA<br>Lys | GGA<br>Gly | TTC<br>Phe | CGG<br>Arg | CAC<br>His | CAG<br>Gln | ACC<br>Thr | ACC<br>Thr | AGA<br>Arg | TTT<br>Phe | TTG<br>Leu | TAT<br>Tyr | CGT<br>Arg | CTG<br>Leu | GTG<br>Val | GGA<br>Gly | 1824 |
|            | 435        |            |            |            |            | 440        |            |            |            |            |            | 445        |            |            |            |      |
| TCA<br>Ser | GAA<br>Glu | GAT<br>Asp | CTG<br>Leu | GCT<br>Ala | GTG<br>Val | GAC<br>Asp | CAA<br>Gln | AGT<br>Ser | ATT<br>Ile | GTC<br>Val | AGC<br>Ser | CCT<br>Pro | TAC<br>Tyr | ACT<br>Thr | TCT<br>Ser | 1872 |
|            | 450        |            |            |            |            | 455        |            |            |            |            | 460        |            |            |            |            |      |
| CGG<br>Arg | ATC<br>Ile | TTG<br>Leu | AAA<br>Lys | CCT<br>Pro | TAT<br>Tyr | ATC<br>Ile | AGG<br>Arg | CGT<br>Arg | GAT<br>Asp | TAT<br>Tyr | GAG<br>Glu | ACA<br>Thr | AAG<br>Lys | CCA<br>Pro | CCC<br>Pro | 1920 |
|            | 465        |            |            |            | 470        |            |            |            |            | 475        |            |            |            |            | 480        |      |
| AAA<br>Lys | CTA<br>Leu | CAG<br>Gln | CTG<br>Leu | CTG<br>Leu | TCC<br>Ser | CAG<br>Gln | ATT<br>Ile | CGC<br>Arg | TCC<br>Ser | CAC<br>His | CTG<br>Leu | CAC<br>His | AAG<br>Lys | AGT<br>Ser | GAC<br>Asp | 1968 |
|            |            |            |            | 485        |            |            |            | 490        |            |            |            |            |            | 495        |            |      |
| CCT<br>Pro | CAC<br>His | TGG<br>Trp | ACA<br>Thr | CCT<br>Pro | GAA<br>Glu | CCT<br>Pro | GAT<br>Asp | GCA<br>Ala | CCT<br>Pro | CTC<br>Leu | GAT<br>Asp | TAC<br>Tyr | TGC<br>Cys | TAT<br>Tyr | GTC<br>Val | 2016 |
|            |            |            | 500        |            |            |            |            | 505        |            |            |            |            | 510        |            |            |      |
| CGA<br>Arg | CCA<br>Pro | AAT<br>Asn | CAC<br>His | ATC<br>Ile | CCA<br>Pro | ACG<br>Thr | ATC<br>Ile | AAC<br>Asn | TCC<br>Ser | ATG<br>Met | TGT<br>Cys | CAG<br>Gln | GAA<br>Glu | TTT<br>Phe | TTC<br>Phe | 2064 |
|            |            | 515        |            |            |            |            | 520        |            |            |            |            | 525        |            |            |            |      |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| TGG CCT GGC ATT GAC CTG TCT GAG TGT CTG CAG TAT CCA GAC TTC AGT<br>Trp Pro Gly Ile Asp Leu Ser Glu Cys Leu Gln Tyr Pro Asp Phe Ser<br>530 535 540     | 2112 |
| GTC GTA GTC CTT TAT AAA AAA GTC ATT GTT GCC TTT GGC TTC ATG GTT<br>Val Val Val Leu Tyr Lys Lys Val Ile Val Ala Phe Gly Phe Met Val<br>545 550 555 560 | 2160 |
| CCC GAT GTG AAG TAC AAC GAA GCT TAC ATT TCA TTT CTG CTT GTT CAT<br>Pro Asp Val Lys Tyr Asn Glu Ala Tyr Ile Ser Phe Leu Leu Val His<br>565 570 575     | 2208 |
| CCC GAG TGG AGG AGA GCA GGG ATT GCC ACG TTC ATG ATC TAT CAT CTG<br>Pro Glu Trp Arg Arg Ala Gly Ile Ala Thr Phe Met Ile Tyr His Leu<br>580 585 590     | 2256 |
| ATT CAG ACG TGC ATG GGC AAG GAT GTG ACT CTT CAC GTC TCG GCG AGC<br>Ile Gln Thr Cys Met Gly Lys Asp Val Thr Leu His Val Ser Ala Ser<br>595 600 605     | 2304 |
| AAC CCT GCC ATG CTG CTG TAC CAG AAG TTT GGC TTC AAG ACA GAG GAG<br>Asn Pro Ala Met Leu Leu Tyr Gln Lys Phe Gly Phe Lys Thr Glu Glu<br>610 615 620     | 2352 |
| TAT GTT TTG GAT TTT TAT GAT AAG TAT TAC CCA CTG GAG AGT ACA GAG<br>Tyr Val Leu Asp Phe Tyr Asp Lys Tyr Tyr Pro Leu Glu Ser Thr Glu<br>625 630 635 640 | 2400 |
| TGT AAA CAT GCA TTC TTC CTG AGG CTC CGA CGC TGAGGTGAAC TCAGTTCTTC<br>Cys Lys His Ala Phe Phe Leu Arg Leu Arg Arg<br>645 650                           | 2453 |
| CCAGCAAACA GCAGATGCTG TCAGAGAGTG GCCTCAGAAG TCGTGCAGGC CCTTCTCCTC                                                                                     | 2513 |
| GAAGTGGGCC CTGGCCTCCT GTGAGTAATG GCCTCCACAG GGTCCAGCTG GGTGAGTGAA                                                                                     | 2573 |
| GCCATGTGCA GAGGTACAAG TGGCTGTTCA ATCCAGAAAC CATCCAGCAG GCCCTGCGTG                                                                                     | 2633 |
| GCCTTCCAGC AGTATCTTGG ACTCCACTGT GGACCAGAAC CAAGTGACTC TGCCATTCTT                                                                                     | 2693 |
| TTTCCACACA ATGAGTGGGC ACAAAGAGC TTCTGAGCTG AAGCATTTGA GAATGGGCCT                                                                                      | 2753 |
| GCTCCTCCTA TGTGAGAGCT CAGGAAGTAT GAAAGATGTT AAAGACTGCC AGGGCCCTCA                                                                                     | 2813 |
| CTGTCTCTGG CCGAGAGGTT ATGAGGTGTC AGGAATGACT CCAACCCTGT CTCAGCCTGT                                                                                     | 2873 |
| GCTGTGCTGT CATCGAACCC CAGAGGATTC ATGGGGCACT GAAGTCCTTT TGTCTCTTAC                                                                                     | 2933 |
| TGACTTTCGT CCTGGTCAGG AAAAAGATAC TCGGTGTCTG TTTCCAGACT GCTGCTGCTT                                                                                     | 2993 |
| TACTTATCTA CCTGTCAGCA CCCCTTGCAG GGACATTGAC CTGGTACAAG AAGTTTACTC                                                                                     | 3053 |
| TTGGCATGGC CTGGAAGTA GCCCGAGAGG AACGGTTGAG CTTGATACAT TAGATGCCTT                                                                                      | 3113 |
| CCCAGGCCCT TCTCATGCTC AGGACAGTTG CACCACAGAA GTGGAGGTGT GGAATGGCGC                                                                                     | 3173 |
| AGGCAGGCCT GGGCGCCCTG TCCACCTCAT GAAGCTGCTT CCTGGGTTGC ACATGTTGGA                                                                                     | 3233 |
| GTTGGACTAC AGGTATCTAA GTGCATTCCA AAAGCATCAG ATATCTCCAA TAAAAATCCT                                                                                     | 3293 |
| TACCATACAA AAA                                                                                                                                        | 3306 |

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 651 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

Met Leu Ala Met Tyr Asn Leu Ser Leu Glu Gly Ser Gly Arg Gln Gly
 1 5 10 15
Tyr Phe Arg Trp Lys Glu Asp Ile Cys Ala Phe Ile Glu Lys His Trp
 20 25 30
Thr Phe Leu Leu Gly Asn Arg Lys Lys Thr Ser Thr Trp Trp Ser Thr
 35 40 45
Val Ala Gly Cys Leu Ser Val Gly Ser Pro Val Tyr Phe Arg Ser Gly
 50 55 60
Ala Gln Glu Phe Gly Glu Pro Gly Trp Trp Lys Leu Val His Asn Arg
 65 70 75 80
Pro Pro Thr Met Arg Pro Glu Gly Glu Lys Leu Ser Ala Ser Thr Leu
 85 90 95
Lys Val Lys Ala Ser Lys Pro Thr Leu Asp Pro Ile Ile Thr Val Glu
 100 105 110
Gly Leu Arg Lys Arg Ala Ser Arg Asn Pro Val Glu Ser Ala Met Glu
 115 120 125
Leu Lys Glu Lys Arg Ser Arg Thr Gln Glu Ala Lys Asp Ile Arg Arg
 130 135 140
Ala Gln Lys Glu Ala Ala Gly Leu Leu Asp Arg Ser Thr Ser Ser Thr
 145 150 155 160
Pro Val Lys Phe Ile Ser Arg Gly Arg Arg Pro Asp Met Ile Leu Glu
 165 170 175
Lys Gly Glu Val Ile Asp Phe Ser Ser Leu Ser Ser Ser Asp Arg Thr
 180 185 190
Pro Leu Thr Ser Pro Ser Pro Ser Pro Ser Leu Asp Phe Ser Ala Pro
 195 200 205
Gly Thr Pro Ala Ser His Ser Ala Thr Pro Ser Leu Leu Ser Glu Ala
 210 215 220
Asp Leu Ile Pro Asp Val Met Pro Pro Gln Ala Leu Phe His Asp Asp
 225 230 235 240
Asp Glu Leu Glu Gly Asp Gly Val Ile Asp Pro Gly Met Glu Tyr Ile
 245 250 255
Pro Pro Pro Ala Gly Ser Ala Ser Gly Leu Met Gly Ser Arg Lys Lys
 260 265 270

```

Val Arg Ala Ala Glu Gln Ile Lys Gln Glu Val Asp Ser Glu Glu Glu  
 275 280 285  
 Lys Pro Asp Arg Met Asp Gly Asp Ser Glu Asp Thr Asp Ser Asn Thr  
 290 295 300  
 Ser Leu His Thr Arg Ala Arg Glu Lys Arg Lys Pro Pro Leu Glu Lys  
 305 310 315 320  
 Asp Thr Lys Pro Lys Gly Pro Arg Tyr Thr Pro Val Ser Ile Tyr Glu  
 325 330 335  
 Glu Lys Leu Leu Leu Lys Arg Leu Glu Ala Cys Pro Gly Ala Val Ala  
 340 345 350  
 Met Thr Pro Glu Ala Arg Arg Leu Lys Arg Lys Leu Ile Val Arg Gln  
 355 360 365  
 Ala Lys Arg Asp Arg Gly Leu Pro Leu Phe Asp Leu Asp Glu Val Val  
 370 375 380  
 Asn Ala Ala Leu Leu Leu Val Asp Gly Ile Tyr Gly Ala Lys Asp Gly  
 385 390 395 400  
 Gly Ala Ser Arg Leu Pro Ala Gly Gln Ala Thr Tyr Arg Thr Thr Cys  
 405 410 415  
 Gln Asp Phe Arg Ile Leu Asp Arg Tyr Gln Thr Ala Leu Pro Ala Arg  
 420 425 430  
 Lys Gly Phe Arg His Gln Thr Thr Arg Phe Leu Tyr Arg Leu Val Gly  
 435 440 445  
 Ser Glu Asp Leu Ala Val Asp Gln Ser Ile Val Ser Pro Tyr Thr Ser  
 450 455 460  
 Arg Ile Leu Lys Pro Tyr Ile Arg Arg Asp Tyr Glu Thr Lys Pro Pro  
 465 470 475 480  
 Lys Leu Gln Leu Leu Ser Gln Ile Arg Ser His Leu His Lys Ser Asp  
 485 490 495  
 Pro His Trp Thr Pro Glu Pro Asp Ala Pro Leu Asp Tyr Cys Tyr Val  
 500 505 510  
 Arg Pro Asn His Ile Pro Thr Ile Asn Ser Met Cys Gln Glu Phe Phe  
 515 520 525  
 Trp Pro Gly Ile Asp Leu Ser Glu Cys Leu Gln Tyr Pro Asp Phe Ser  
 530 535 540  
 Val Val Val Leu Tyr Lys Lys Val Ile Val Ala Phe Gly Phe Met Val  
 545 550 555 560  
 Pro Asp Val Lys Tyr Asn Glu Ala Tyr Ile Ser Phe Leu Leu Val His  
 565 570 575  
 Pro Glu Trp Arg Arg Ala Gly Ile Ala Thr Phe Met Ile Tyr His Leu  
 580 585 590  
 Ile Gln Thr Cys Met Gly Lys Asp Val Thr Leu His Val Ser Ala Ser  
 595 600 605

Asn Pro Ala Met Leu Leu Tyr Gln Lys Phe Gly Phe Lys Thr Glu Glu  
 610 615 620  
 Tyr Val Leu Asp Phe Tyr Asp Lys Tyr Tyr Pro Leu Glu Ser Thr Glu  
 625 630 635 640  
 Cys Lys His Ala Phe Phe Leu Arg Leu Arg Arg  
 645 650

## (2) INFORMATION FOR SEQ ID NO:28:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

## (vii) IMMEDIATE SOURCE:

(B) CLONE: HW041

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 3407..3482
- (D) OTHER INFORMATION: /label= SAC\_24317

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GTCGACCCTC CTTCTGCCCT GGCTCCTGTT GATGAGCACA GTGCCGTCCC TGATCAGTTC | 60  |
| TTTCTTCCTG TGAATTTGCT TCGTAGCCCA TCAGGCTGGT AGACTGGCAG CACGGTCAGT | 120 |
| GTCACACGAG GGACAGGACT TCCCTGAAGT GAAGCAGCAA TGTCATGGAA GCAAACCCCT | 180 |
| GTGAGCGAGA GACAGGCCCC GAGGCTGCTG CCACAAGGTC TCATGTTCAT TGCTGGGGAC | 240 |
| ACTAGCTTCC TACAAACCCC AGGAGACGCT GCCCATAGCA CGGGTGGCCC TTCAGGCTCC | 300 |
| TGAACTATCT ATCCCCAGAT CAGTAGGATT TGTTTTCCAA GTCCCCTTCC TCATTCCTTC | 360 |
| TTTGCTCAAG AGAAAAAAGA AAAGTGGTAA CTCTGTGACT CTAAGTCCCT CTTAAATGCA | 420 |
| GCGCTGAATC TAGCTTGGCT CGGAGATCTC TGACTTGTCC CTAGGGTGAG ACTGTGGCCT | 480 |
| CCCCAGGTTG AGGTGGCACG TGTATTGTGA GAGATTAGCC TGGAGAGCAG AGAAGGGGGG | 540 |
| AGGGGGGATA GGGAGGAGAG AGCAATCGTG TCTCCCTACA GGACCCTGGG CCATCTGACA | 600 |
| AGACAGAGGA GGTGGGACTG GCTTCCCCAT GCTGCACATG GCAGTGGGAA CCAGGCTTGG | 660 |
| AGTCCCCCAC CCCCTCCTTA CCTCTTCTCT CAGACCTTGT AGCCCTAGCT TGCCCTGTGC | 720 |
| TCTGCAGGGA AGGGGATGAG AGGACAGCAT AAGAAGTCTT GCCAGTTGAG GTGGGGCTGG | 780 |
| AAGATGAAGC AGGTGGGTGT AGGAATCATT TTGGATAGGG CATGTTGTTT GGTGACGGC  | 840 |
| AACTAATTCT CTTAAGAGCA TATTGTCTCC AGTTAATGTT GGAGACAACC CAGAAAGGGA | 900 |

|            |            |            |            |             |            |      |
|------------|------------|------------|------------|-------------|------------|------|
| AGGGTATAGA | GATGGGTAAT | TAATGAGATA | TTCCAGCCCT | GGAGCAATGT  | CTGAGCCACC | 960  |
| CCAAACTTAG | GCTGTCTCCC | AGCATAGGAG | TGGGGCACTG | CCCCTTACTC  | AAATTCTAGT | 1020 |
| CTAAGTGTTT | CAGACACATT | GTACACTTGG | ACAGGAAATC | TCCTGTTCCT  | GCATACCCTC | 1080 |
| TCCCCCATA  | CCTCTCCCCC | ATACCCCTC  | CCCCATACCT | TCTCCCCCAT  | ACTGTTAGTA | 1140 |
| CGTTTCAGTT | GTTCAAAAGC | AAAGGGGGCG | CAGACTAGGC | TTTAACTGCA  | TGTGGAGTGT | 1200 |
| AGATTTTGCC | TAAGAATCCA | TGTTGAAGAA | GAGAGAGGCT | ATGTCTTTAA  | GGTCGAGGCC | 1260 |
| CTTCAGTCTT | CTGTCTTGT  | AATTCCTTG  | AAGCGTGAGC | CCCAGGCACT  | CAGAAGCCAT | 1320 |
| GTTGTACTCC | GGGAAGTTCA | TGGGACCTGA | ACTCCTTCAA | CACCGGGAAC  | AACAGTACTG | 1380 |
| CATAGGTACT | TTGGTACTGA | CTGTGCAAGC | ACTAGAAAAA | GTACCCGTTG  | AATGGCCCTC | 1440 |
| ACAGCATCAG | GGAAACGAGG | CCGAGTTCAC | TCTCCTGATT | GCTCAGATGC  | AGAAGCTGGA | 1500 |
| CCCGTGAGGT | GTACCAGCCC | ACCTCCAAGC | TTGACACAGA | GGCTAGCACT  | TAAAGCAAAG | 1560 |
| ACTCAGAAGA | GGAGTCTCAG | TCACAGGCTG | CACAGCCTTG | AACATGATAT  | CTAGAACTAT | 1620 |
| GCCTGGGTGA | TCGGTGGCCC | AACTTGTGAC | ACTTGTGTGC | ACATAGGGAA  | GCTGACGCTC | 1680 |
| CTCTCGGGGC | CTGAAAACAG | GACTAAACCC | AAACCCATA  | TAACCTAACCA | TACCACTGCC | 1740 |
| ATCCACAGGC | GTGGATGGAA | GTCTTCACGG | TCTGTTACAA | GCACAAGTAC  | AAAGCCGATA | 1800 |
| AAAATAAGTC | AAAGCCCTTC | CTCGTGGTGC | AGAGGGCTCC | TCCTCAGATC  | TCTTGGAGCC | 1860 |
| TTTGATCATA | GAGCTTGACG | GTCTCCTCTC | GGGATAAAGG | ACAGGTAAAG  | GCTGTGGCCT | 1920 |
| TCAGCGGTGA | CTGCCCCACA | CCCTGCTTTC | CTTAGGGGTG | GAGACAAGGA  | ATGGTGGGGC | 1980 |
| CAGTGTGTGT | CAGAGAGAAG | TCTCTCTTTG | GAGCCCATGT | ATGGGGCTTG  | ACCTTTTGCT | 2040 |
| GTGAGTGCAT | TTAGAGGCAA | GTGAATCTTG | GCCTCAGTAC | AGAGAACCCA  | GCGGTTTCAG | 2100 |
| CACTCAAGAA | AGAAGCCGCA | GTGTCCCTTA | CAGAGAGGCT | CTGTCTTGCT  | TGGCCCCAGC | 2160 |
| CACCTGCGCC | ACACATTTAA | TAAAGTGGCT | GAAACTCCTC | CTTTCCAAGA  | GCTAGTGTGC | 2220 |
| TGGGTCTGT  | CCTCCCCACA | GCCTTCTGAG | TCCCAGAGAC | TTGTGTGAGC  | AGTCGGATAA | 2280 |
| GGCCAATCTG | GGAGACAGGG | GATGACCATG | ACACAAGGTG | TTTCCAGGCA  | GGTCCCTTGT | 2340 |
| GCGTAGGCTG | CAGAGAGCTG | TCCTGACTGG | GAGCTTGGGT | TGTACGAACA  | CATGGTGCCT | 2400 |
| TCTTTGTCTG | TGCTGAACGA | GTAGGGTGTG | TTTCTCTGTG | TTCTCTGAGT  | AAGATCACAC | 2460 |
| CCTCTTTAAG | CAAAGGGGTG | TTGTGGATAT | TAGAAGCAAG | ATTGATAAAT  | GTTCTTAAAT | 2520 |
| GGTGGTGCTA | GAGAAAAGTC | AGTCCCCGTA | ACTTCCTAAA | AGCTGAGTCA  | GCCAGTCTCT | 2580 |
| AAGTATGTAC | ATGTTGGCTT | TCTTCTATTT | TTTTTCTAGT | TAATCAGTGT  | GTTTAAATG  | 2640 |
| TTTTTAGTTG | ATGTGAGGAT | TTTTTTAAAG | GCATTTGTGT | GTGGTGTGGC  | TCCATGGGAG | 2700 |
| ATAGGCTGTG | TAATAAGAAC | CCTCAGAAGC | CAGCCAGTCA | TCCAAGGGGC  | GCCCAAGTTC | 2760 |
| AGTGGATTTC | TTCAGGAATT | GGAGAGCAGT | ATTTTTCCTT | CTTTTCAGTA  | GTATGCCTGT | 2820 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| TCTCATTTAG TAATTTAATG GTATATTGCA TTATATGTGA ATGCATACAT AAACGGTGGA  | 2880 |
| ATTTCTCTTA ATATCCAAAA AAGTCCTTCT GTTGCCCTCT GAGCTCTCTC CTTGGGGAGG  | 2940 |
| ACTGCAGGGC TCACTGTGTA AAATGGTTGT GGACTCCTCT AGCAGAAATGG CTTCCAAGGC | 3000 |
| CTGGCCCATT CCTCAGATTC CCTTTGAAGT GAGAGGTCAT TGTCTTTTGA GAATGGATTT  | 3060 |
| AAGTTTTTGA AATACCCAC GCTGTTTACA GTGCAAGCGA CTGAACACAG AACAATTAGT   | 3120 |
| CAGAATCAGA ATCCCAGGGC CATCAAGATG ACTCCACGGA AAAGGGACTG CCACCAACCA  | 3180 |
| GAGCCAAGAC CTGAGTTTGG TCCCCAGGAA CCCCATGGCA GCAGGAGAGA GTCAGCCGAT  | 3240 |
| GCAAGTGTCA CACACACACA TAAACACACA CATAACATG CAACACATAC ACACAAACAC   | 3300 |
| ATACATACAC ACACACAAAC ACATACACAC ATGCACACAC ACACACACAC ACACACACAC  | 3360 |
| AGAGTTTTTG GAAGAATATC TATGATGTAG GAAAAGGTTT GTTAGTACCT GCAACCTCTA  | 3420 |
| GGGCCTCAT TCCAAGCCTG CTGCTTCTCT TGCCAGGACT TATACGTGTG CAACCCCTGC   | 3480 |
| GTACACTACA GACCTAAGTA CATACTCGCT AACATGAACA CCCAGTAGGT ATTCTGTAAA  | 3540 |
| ACGGATATAC TTAAGTGCAT GTTATTGTCTG TGTGTGCCGC GACTGAGCTG TGTCTTTGTC | 3600 |
| ATGAAACTTT GCTTCTTTGC CAAATTAAGA CTCTGCCCTC CCTCCGAGGA AGGAAATATA  | 3660 |
| CAGCAGTTTC TGAATCAGC TTCTCAAGTT TTCCCGCCTG TGTGTGTGTT ACTTGTGGCT   | 3720 |
| TTGCCTGAGA GTCTGTCTC ACGTACACAC CTGTGAGTAT TTATTACAAG GCAGAACGGG   | 3780 |
| GACAGGCGTA GCCATAGTAC TTGTGTTTGA ATGTTTCCAG GGAGGGACAA TGGAGCCCCC  | 3840 |
| TCCTCAGTGA GGTGCTCACA GAATCTGTGT CAAATTCGTG GAACGGGGTC CAACACTAGT  | 3900 |
| ACCAGCTTCA CCCCACCCT GAGTGCCCTG GAGCCACTGC CCTCTCTACT GCCTTGTGTG   | 3960 |
| TGCATGGGTG TGGTTGTGTG TGTCTCTGTT GGGGCATGTG CCGCATTTCTG CAGTGGAATT | 4020 |
| TGGTATCCAC ATGTAACCTT TGGCATCTGT GTTCCCTGGAC CGCATTGACA GATCTGTGGT | 4080 |
| GTGCAGATCT GTGTAGATGG GTCTGTGTGC AAAGTGGGGA GTCCCCTGAA AGTGAATATG  | 4140 |
| GATATTGTTG GTCAGCCAAA GACTTTCCTA TTCTTTGCTG CTTAAACTTT GTGCCTTAAT  | 4200 |
| ATTGTAAATA TAAACGGTTA AAACAAAAGT CGAC                              | 4234 |

## (2) INFORMATION FOR SEQ ID NO:29:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1792 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (vii) IMMEDIATE SOURCE:



(B) CLONE: HW042

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 8..889

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: complement (1409..1618)

(D) OTHER INFORMATION: /label= SAC\_24017

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

|         |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GTCGACC | AAG | GAT | GGT | GGA | AGT | TTC | AGT | GGT | ACT | GGT | GGC | CTT | CCA | GAT | 49  |     |
|         | Lys | Asp | Gly | Gly | Ser | Phe | Ser | Gly | Thr | Gly | Gly | Leu | Pro | Asp |     |     |
| 1       |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     |     |
| TAT     | TCT | GCC | CCC | AAT | CCC | ATT | AAA | GTG | ACC | CAT | CGG | TGC | TAC | ATC | CTT | 97  |
| Tyr     | Ser | Ala | Pro | Asn | Pro | Ile | Lys | Val | Thr | His | Arg | Cys | Tyr | Ile | Leu |     |
| 15      |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| GAG     | AAT | GAC | ACA | GTC | CAG | TGT | GAC | TTG | GAC | CTG | TAC | AAG | TCC | CTG | CAG | 145 |
| Glu     | Asn | Asp | Thr | Val | Gln | Cys | Asp | Leu | Asp | Leu | Tyr | Lys | Ser | Leu | Gln |     |
|         |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| GCT     | TGG | AAA | GAC | CAC | AAA | TTG | CAC | ATC | GAC | CAT | GAG | ATT | GAA | ACC | CTG | 193 |
| Ala     | Trp | Lys | Asp | His | Lys | Leu | His | Ile | Asp | His | Glu | Ile | Glu | Thr | Leu |     |
|         |     |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| CAG     | AAC | AAA | ATT | AAG | AAC | CTT | CGA | GAA | GTC | AGG | GGT | CAC | CTG | AAG | AAG | 241 |
| Gln     | Asn | Lys | Ile | Lys | Asn | Leu | Arg | Glu | Val | Arg | Gly | His | Leu | Lys | Lys |     |
|         |     |     |     | 65  |     |     | 70  |     |     |     |     | 75  |     |     |     |     |
| AAG     | CGG | CCA | GAA | GAA | TGT | GAC | TGT | CAC | AAA | GTC | AGT | TAC | CAC | AGC | CAA | 289 |
| Lys     | Arg | Pro | Glu | Glu | Cys | Asp | Cys | His | Lys | Val | Ser | Tyr | His | Ser | Gln |     |
|         |     |     |     | 80  |     |     | 85  |     |     |     |     | 90  |     |     |     |     |
| CAC     | AAA | GGC | CGC | CTC | AAG | CAC | AAG | GGC | TCC | AGC | CTG | CAC | CCT | TTC | AGG | 337 |
| His     | Lys | Gly | Arg | Leu | Lys | His | Lys | Gly | Ser | Ser | Leu | His | Pro | Phe | Arg |     |
|         |     |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| AAG     | GGT | CTG | CAG | GAG | AAA | GAC | AAG | GTG | TGG | CTG | TTG | CGG | GAG | CAG | AAA | 385 |
| Lys     | Gly | Leu | Gln | Glu | Lys | Asp | Lys | Val | Trp | Leu | Leu | Arg | Glu | Gln | Lys |     |
|         |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| CGC     | AAG | AAG | AAA | CTG | CGC | AAG | CTG | CTG | AAG | CGA | CTG | CAG | AAC | AAT | GAC | 433 |
| Arg     | Lys | Lys | Lys | Leu | Arg | Lys | Leu | Leu | Lys | Arg | Leu | Gln | Asn | Asn | Asp |     |
|         |     |     |     | 130 |     |     | 135 |     |     |     |     |     | 140 |     |     |     |
| ACG     | TGC | AGC | ATG | CCG | GGC | CTC | ACG | TGC | TTT | ACT | CAC | GAC | AAC | CAC | CAC | 481 |
| Thr     | Cys | Ser | Met | Pro | Gly | Leu | Thr | Cys | Phe | Thr | His | Asp | Asn | His | His |     |
|         |     |     |     | 145 |     |     | 150 |     |     |     |     | 155 |     |     |     |     |
| TGG     | CAG | ACC | GCG | CCG | CTC | TGG | ACG | TTG | GGA | CCC | TTC | TGC | GCC | TGC | ACC | 529 |
| Trp     | Gln | Thr | Ala | Pro | Leu | Trp | Thr | Leu | Gly | Pro | Phe | Cys | Ala | Cys | Thr |     |
|         |     |     |     | 160 |     |     | 165 |     |     |     | 170 |     |     |     |     |     |
| AGC     | GCC | AAC | AAT | AAC | ACG | TAC | TGG | TGC | CTG | CGG | ACC | ATC | AAC | GAG | ACC | 577 |
| Ser     | Ala | Asn | Asn | Asn | Thr | Tyr | Trp | Cys | Leu | Arg | Thr | Ile | Asn | Glu | Thr |     |
|         |     |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |
| CAC     | AAC | TTC | CTC | TTC | TGT | GAA | TTC | GCA | ACT | GGC | TTC | ATA | GAA | TAC | TTT | 625 |

|            |            |             |             |             |            |     |     |            |            |            |     |     |     |     |     |      |
|------------|------------|-------------|-------------|-------------|------------|-----|-----|------------|------------|------------|-----|-----|-----|-----|-----|------|
| His        | Asn        | Phe         | Leu         | Phe         | Cys        | Glu | Phe | Ala        | Thr        | Gly        | Phe | Ile | Glu | Tyr | Phe |      |
|            |            |             |             | 195         |            |     |     |            | 200        |            |     |     |     | 205 |     |      |
| GAC        | CTC        | AGT         | ACG         | GAC         | CCC        | TAC | CAG | CTG        | ATG        | AAC        | GCG | GTC | AAC | ACA | CTG | 673  |
| Asp        | Leu        | Ser         | Thr         | Asp         | Pro        | Tyr | Gln | Leu        | Met        | Asn        | Ala | Val | Asn | Thr | Leu |      |
|            |            |             | 210         |             |            |     |     | 215        |            |            |     |     | 220 |     |     |      |
| GAC        | AGG        | GAC         | GTT         | CTC         | AAC        | CAG | CTG | CAC        | GTC        | CAG        | CTC | ATG | GAG | CTA | AGG | 721  |
| Asp        | Arg        | Asp         | Val         | Leu         | Asn        | Gln | Leu | His        | Val        | Gln        | Leu | Met | Glu | Leu | Arg |      |
|            |            |             | 225         |             |            |     | 230 |            |            |            |     | 235 |     |     |     |      |
| AGC        | TGC        | AAA         | GGC         | TAC         | AAG        | CAG | TGT | AAC        | CCC        | CGG        | ACC | CGC | AAT | ATG | GAC | 769  |
| Ser        | Cys        | Lys         | Gly         | Tyr         | Lys        | Gln | Cys | Asn        | Pro        | Arg        | Thr | Arg | Asn | Met | Asp |      |
|            |            |             | 240         |             |            | 245 |     |            |            |            | 250 |     |     |     |     |      |
| CTG        | GGG        | CTT         | AGA         | GAC         | GGA        | GGA | AGC | TAT        | GAG        | CAA        | TAC | AGG | CAG | TTT | CAG | 817  |
| Leu        | Gly        | Leu         | Arg         | Asp         | Gly        | Gly | Ser | Tyr        | Glu        | Gln        | Tyr | Arg | Gln | Phe | Gln |      |
|            | 255        |             |             |             | 260        |     |     |            |            | 265        |     |     |     |     | 270 |      |
| CGT        | CGA        | AAA         | TGG         | CCA         | GAA        | ATG | AAG | AGA        | CCC        | TCT        | TCC | AAA | TCA | CTG | GGA | 865  |
| Arg        | Arg        | Lys         | Trp         | Pro         | Glu        | Met | Lys | Arg        | Pro        | Ser        | Ser | Lys | Ser | Leu | Gly |      |
|            |            |             |             | 275         |            |     |     |            | 280        |            |     |     |     | 285 |     |      |
| CAG        | CTA        | TGG         | GAA         | GGT         | TGG        | GAA | GGC | TAATCGGCCA | TGGAGAGGAA | CCTCCAAAAC |     |     |     |     |     | 919  |
| Gln        | Leu        | Trp         | Glu         | Gly         | Trp        | Glu | Gly |            |            |            |     |     |     |     |     |      |
|            |            |             | 290         |             |            |     |     |            |            |            |     |     |     |     |     |      |
| CAGAGGCCTC | CTGTGGCTGC | CCAGGCGTGC  | AAAAATCACC  | CAATTCCGAG  | GAGATCGATG |     |     |            |            |            |     |     |     |     |     | 979  |
| CTGGAAGTGG | GAGACTTGAC | AGGAGGCAGG  | GTCTGCAC TT | GGGACAGGAA  | ATCCCGAGGA |     |     |            |            |            |     |     |     |     |     | 1039 |
| GAACGCCAAG | ACTTCCAGAG | GCTCATTGTT  | TTGCCCCGCT  | TTGCTTCGGA  | TTGAACCTCA |     |     |            |            |            |     |     |     |     |     | 1099 |
| CCGGCCGCAC | AAGGATGCGT | CCTGACACCT  | GGAGTCTCCG  | CTCACCC TTT | CAGAGGCTCA |     |     |            |            |            |     |     |     |     |     | 1159 |
| CCAAGACAAA | GGAAGTAATT | CCCATGGACT  | TTCTCTCCAGA | GATGGAAATT  | GCTGGGATTT |     |     |            |            |            |     |     |     |     |     | 1219 |
| ACCCATCCCC | TCCCCTGTAC | CCCCTTCCCC  | ACTAGGGAAA  | CAAGCTTGTT  | TTAACCTTCT |     |     |            |            |            |     |     |     |     |     | 1279 |
| TATTCTTTGG | AGAAAGCACG | GATGTCCCAG  | GTGCTGTCAA  | CAGCGCAGTC  | TTGACAATGG |     |     |            |            |            |     |     |     |     |     | 1339 |
| TCTATAGCAC | AAAACAGTAC | CATTACACCTG | GCTGGATGAG  | CCGGCTGCCC  | CAGAAGCTGC |     |     |            |            |            |     |     |     |     |     | 1399 |
| CTTCACTGTA | CATATGTGAC | TGCTCACATG  | TAACCAACAC  | AGGGACTTGT  | AGGGGGAATC |     |     |            |            |            |     |     |     |     |     | 1459 |
| TCACTAATAC | GAAATCCCAT | TTTCAAGAGT  | CGCGGTGTCA  | ATAAACACTC  | TGTGGCTGGT |     |     |            |            |            |     |     |     |     |     | 1519 |
| GTCAAGGGTA | ATCCCTTGAG | CTTTCAGACA  | TTTCTGTTCC  | TGCCCAGGAT  | TCGTTCTCTT |     |     |            |            |            |     |     |     |     |     | 1579 |
| GTTATCCATA | TCCATCCCAG | AACTGATGTT  | TTCTAAGGTA  | CTGAAACCCC  | AAGTTGATGT |     |     |            |            |            |     |     |     |     |     | 1639 |
| GTGTCCTGTG | TTTAAATGAC | ATTGTATTTG  | TAAAGCAATT  | TTGTAGTATA  | AAAGTACCAT |     |     |            |            |            |     |     |     |     |     | 1699 |
| CTTCCAGTGT | TCACATCCCC | CCCAGCCAAT  | GACTAGCTCT  | TGGTATGAAA  | AAAAAAATCT |     |     |            |            |            |     |     |     |     |     | 1759 |
| TTGAATTTTT | GTAAAAAAA  | AAAAAAAGTC  | GAC         |             |            |     |     |            |            |            |     |     |     |     |     | 1792 |

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Lys Asp Gly Gly Ser Phe Ser Gly Thr Gly Gly Leu Pro Asp Tyr Ser  
 1 5 10 15  
 Ala Pro Asn Pro Ile Lys Val Thr His Arg Cys Tyr Ile Leu Glu Asn  
 20 25 30  
 Asp Thr Val Gln Cys Asp Leu Asp Leu Tyr Lys Ser Leu Gln Ala Trp  
 35 40 45  
 Lys Asp His Lys Leu His Ile Asp His Glu Ile Glu Thr Leu Gln Asn  
 50 55 60  
 Lys Ile Lys Asn Leu Arg Glu Val Arg Gly His Leu Lys Lys Lys Arg  
 65 70 75 80  
 Pro Glu Glu Cys Asp Cys His Lys Val Ser Tyr His Ser Gln His Lys  
 85 90 95  
 Gly Arg Leu Lys His Lys Gly Ser Ser Leu His Pro Phe Arg Lys Gly  
 100 105 110  
 Leu Gln Glu Lys Asp Lys Val Trp Leu Leu Arg Glu Gln Lys Arg Lys  
 115 120 125  
 Lys Lys Leu Arg Lys Leu Leu Lys Arg Leu Gln Asn Asn Asp Thr Cys  
 130 135 140  
 Ser Met Pro Gly Leu Thr Cys Phe Thr His Asp Asn His His Trp Gln  
 145 150 155 160  
 Thr Ala Pro Leu Trp Thr Leu Gly Pro Phe Cys Ala Cys Thr Ser Ala  
 165 170 175  
 Asn Asn Asn Thr Tyr Trp Cys Leu Arg Thr Ile Asn Glu Thr His Asn  
 180 185 190  
 Phe Leu Phe Cys Glu Phe Ala Thr Gly Phe Ile Glu Tyr Phe Asp Leu  
 195 200 205  
 Ser Thr Asp Pro Tyr Gln Leu Met Asn Ala Val Asn Thr Leu Asp Arg  
 210 215 220  
 Asp Val Leu Asn Gln Leu His Val Gln Leu Met Glu Leu Arg Ser Cys  
 225 230 235 240  
 Lys Gly Tyr Lys Gln Cys Asn Pro Arg Thr Arg Asn Met Asp Leu Gly  
 245 250 255  
 Leu Arg Asp Gly Gly Ser Tyr Glu Gln Tyr Arg Gln Phe Gln Arg Arg  
 260 265 270  
 Lys Trp Pro Glu Met Lys Arg Pro Ser Ser Lys Ser Leu Gly Gln Leu  
 275 280 285  
 Trp Glu Gly Trp Glu Gly  
 290

## (2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2261 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: HW043

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 8..634

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 582..808  
 (D) OTHER INFORMATION: /label= SAC\_24533

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

|         |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GTCGACG | GCT | CCA | CCA | GGT | TCA | AGA | CAC | AAA | CCT | GTG | CCT | ACC | AAG | TCA | 49  |
| Ala     | Pro | Pro | Gly | Ser | Arg | His | Lys | Pro | Val | Pro | Thr | Lys | Ser |     |     |
| 1       |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     |     |
| ACA     | CCA | GCT | GGC | ACA | GAA | CTA | GGT | AGC | ACA | GGA | AGC | GAC | GGG | GGA | 97  |
| Thr     | Pro | Ala | Gly | Thr | Glu | Leu | Gly | Ser | Thr | Gly | Ser | Asp | Gly | Gly | Asp |
| 15      |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| GCA     | GTA | GAA | TAC | AAC | CCC | AAC | CTC | CTG | GAT | GAC | CCA | CAG | TGG | CCG | 145 |
| Ala     | Val | Glu | Tyr | Asn | Pro | Asn | Leu | Leu | Asp | Asp | Pro | Gln | Trp | Pro | Cys |
|         |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |
| GGG     | AAG | CAC | AAG | CGT | GTA | CTC | ATC | TTT | GCC | TCA | TAC | ATG | ACC | ACT | 193 |
| Gly     | Lys | His | Lys | Arg | Val | Leu | Ile | Phe | Ala | Ser | Tyr | Met | Thr | Thr | Val |
|         |     |     | 50  |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| ATA     | GAG | TAT | GTG | AAG | CCT | GCA | GAC | CTC | AAA | AAG | GAC | ATG | AAC | GAG | 241 |
| Ile     | Glu | Tyr | Val | Lys | Pro | Ala | Asp | Leu | Lys | Lys | Asp | Met | Asn | Glu | Thr |
|         |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |
| TTC     | AGG | GAG | AAG | TTC | CCT | CAT | ATC | AAA | CTG | ACA | TTG | AGC | AAA | ATT | 289 |
| Phe     | Arg | Glu | Lys | Phe | Pro | His | Ile | Lys | Leu | Thr | Leu | Ser | Lys | Ile | Arg |
|         | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |
| AGT     | TTA | AAA | CGG | GAG | ATG | CGG | AAC | CTT | TCT | GAA | GAG | TGC | AGC | TTG | 337 |
| Ser     | Leu | Lys | Arg | Glu | Met | Arg | Asn | Leu | Ser | Glu | Glu | Cys | Ser | Leu | Glu |
| 95      |     |     |     | 100 |     |     |     |     |     | 105 |     |     |     | 110 |     |
| CCT     | GTG | ACT | GTG | TCC | ATG | GCC | TAT | GTG | TAC | TTT | GAG | AAG | CTT | GCA | 385 |
| Pro     | Val | Thr | Val | Ser | Met | Ala | Tyr | Val | Tyr | Phe | Glu | Lys | Leu | Ala | Leu |
|         |     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |
| CAG     | GGC | AAG | CTC | AAC | AAA | CAG | AAC | CGC | AAA | CTG | TGT | GCT | GGC | GCC | 433 |
| Gln     | Gly | Lys | Leu | Asn | Lys | Gln | Asn | Arg | Lys | Leu | Cys | Ala | Gly | Ala | Cys |
|         |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GTT CTG TTG GCT GCC AAG ATC AGC AGT GAC CTC CGC AAG AGT GAA GTG<br>Val Leu Leu Ala Ala Lys Ile Ser Ser Asp Leu Arg Lys Ser Glu Val<br>145 150 155     | 481  |
| AAG CAG CTT ATT GAC AAG CTG GAG GAA AGG TTC CGG TTC AAC AGG AAG<br>Lys Gln Leu Ile Asp Lys Leu Glu Glu Arg Phe Arg Phe Asn Arg Lys<br>160 165 170     | 529  |
| GAT CTC ATT GGA TTT GAG TTC ACG GTG CTT GTG GCT TTG GAA CTG GCC<br>Asp Leu Ile Gly Phe Glu Phe Thr Val Leu Val Ala Leu Glu Leu Ala<br>175 180 185 190 | 577  |
| CTG TAC CTC CCG GAG AAC CAA GTA TTA CCT CAC TAC AGA CGC CTC ACC<br>Leu Tyr Leu Pro Glu Asn Gln Val Leu Pro His Tyr Arg Arg Leu Thr<br>195 200 205     | 625  |
| CAG CAG TTC TAGCCCAGAA CAGTGCACCC CACAGGGAGC CTGCTTTGGC<br>Gln Gln Phe                                                                                | 674  |
| AGGAAGGCGA GTAGCTTGGC TAGAGCACTG ACTAGTAGTG TCCCTGTCCT TCCTCTAGTA                                                                                     | 734  |
| ACTGCACTTG CCCCTCAGTC CAGGGCTGCA CTTAGCTTCC CTTGGAAAGA GGCACTGCTC                                                                                     | 794  |
| TTATTTTGGG GTGTACCCCA TCTTCACCTT GAGGCCCTGT TGAGGGT TTT CCTGAAGCAA                                                                                    | 854  |
| ATGAACATCG TGGGGCTTGG TTTGCTTTTC ATGTGCCTGA GACCAGCCTG GTTTATGTTG                                                                                     | 914  |
| TCAATCCTGA GGTCCAGCTT TCATTTTGCC TAGCCATGAA ACCATTCTCTG TAGAGACCTA                                                                                    | 974  |
| GGTGTCCAGA CCTTCTGAAC ATACTGGAAT TGCCAGGCTT CTGTCTCCTG GTGCCCTCCAC                                                                                    | 1034 |
| CCAGGCAGAG CTCCCCCATC AGCACTTTTT TTTGGTCAAG ATGCAGGAAA GGGCAGTCTG                                                                                     | 1094 |
| CTCACACTGG ACCTTGTTAA AGCATCTGCC ACTGTGAAAC CCCTGTGCCA CCACATACAG                                                                                     | 1154 |
| TGTTTGGCCA ACACCACCAC CCACCCCAAC CCCTGCCTCC TGCCAGCACT TATCCCTGCG                                                                                     | 1214 |
| GTACTGGACC ATTTAAGACA ACCGCTGACT GCGGGCTCTT GACTTTCTCTG AGCAATATCA                                                                                    | 1274 |
| TGATGGAGAA AAGGTATTAA CTTGAGATTT GGTTCCTATA ACAGAAAAGA CGGCCCATTA                                                                                     | 1334 |
| AGGCCTGCTG CTGACTCTGC ACCACACTTG ATCCTCAAGC AGGAAGGTAC TGACCCTGCC                                                                                     | 1394 |
| ACCTAACAGC ACATCAGTGA CTCCTCACAA ATAGATGCCA TCCAGGCCAA CTTGCCTGTG                                                                                     | 1454 |
| TATTGACTGT GCCACTGTCT TCCTACTGGC ACCAGACAAG AGCCATCCTC CACCTTCCCA                                                                                     | 1514 |
| GGCCTGTTAT TCCCTACAAC TGGTCACCAG CCTGGCAGAT GCCAGTCCCA CTGCTCTCAA                                                                                     | 1574 |
| GTGCTTGGTT CCACAGCCAC TCATCCCAGA AATGCTTACC CTCTCAAGCC TGACACCACT                                                                                     | 1634 |
| CAACTACCTA ATGGATGTTA GTAGCTTAAA CAGAGACCTT GAAGGATAGT AGAAGGATAG                                                                                     | 1694 |
| TAAACTCTAG CCTTCTACCC TGCCCATGCT TATGCTGGTG TAAGCACGCT ATCCTTAGAG                                                                                     | 1754 |
| CACCTGGGTG CCATCTGCAG ACAGTGATGT CTTACTTAAA ATGAACCTTA GATACAGCTG                                                                                     | 1814 |
| ACTGGTCGGC TATCCCTGGG GGTGATACCC TGGTAGCTTA TTCTAGTTAT GTTAAAGCTG                                                                                     | 1874 |
| GCAACAGTGA TAATTTAAGC TTCTATATTT ATGATCTTAC CAAGCTGGTG TGCTGTAGT                                                                                      | 1934 |

CCTTCCCTCC TTGCCCTCAG TAATGCTAAG AGCTGCTGAC ATGTGGTATG ATAAGCACTG 1994  
 TTACAACAAA ACCAACCTTT AAACCAAATG ACAGGCTAAA CACAGTGTCT GTCCTAGACT 2054  
 AAGTCCAGAA ATCCGAGGTG TGCCACGGT GTCCAGCTGG ACTGTGACCC AATGCCACAG 2114  
 ACCTGGTGCT GTACCTTCAG CACTCAACAG GCACAGCTGT GTGTGTGACC TCAGAATGCT 2174  
 GCTTATGTAT GTCCAGCCGG TTCTGAATGG AAGGTGTTAA ATGTTTTTGT TAAAAGTAA 2234  
 ACTTGTTTTT GCAAAAAAAA AGTCGAC 2261

## (2) INFORMATION FOR SEQ ID NO:32:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Pro | Gly | Ser | Arg | His | Lys | Pro | Val | Pro | Thr | Lys | Ser | Thr | Pro | 1   | 5   | 10  | 15  |
| Ala | Gly | Thr | Glu | Leu | Gly | Ser | Thr | Gly | Ser | Asp | Gly | Gly | Asp | Ala | Val | 20  | 25  | 30  |     |
| Glu | Tyr | Asn | Pro | Asn | Leu | Leu | Asp | Asp | Pro | Gln | Trp | Pro | Cys | Gly | Lys | 35  | 40  | 45  |     |
| His | Lys | Arg | Val | Leu | Ile | Phe | Ala | Ser | Tyr | Met | Thr | Thr | Val | Ile | Glu | 50  | 55  | 60  |     |
| Tyr | Val | Lys | Pro | Ala | Asp | Leu | Lys | Lys | Asp | Met | Asn | Glu | Thr | Phe | Arg | 65  | 70  | 75  | 80  |
| Glu | Lys | Phe | Pro | His | Ile | Lys | Leu | Thr | Leu | Ser | Lys | Ile | Arg | Ser | Leu | 85  | 90  | 95  |     |
| Lys | Arg | Glu | Met | Arg | Asn | Leu | Ser | Glu | Glu | Cys | Ser | Leu | Glu | Pro | Val | 100 | 105 | 110 |     |
| Thr | Val | Ser | Met | Ala | Tyr | Val | Tyr | Phe | Glu | Lys | Leu | Ala | Leu | Gln | Gly | 115 | 120 | 125 |     |
| Lys | Leu | Asn | Lys | Gln | Asn | Arg | Lys | Leu | Cys | Ala | Gly | Ala | Cys | Val | Leu | 130 | 135 | 140 |     |
| Leu | Ala | Ala | Lys | Ile | Ser | Ser | Asp | Leu | Arg | Lys | Ser | Glu | Val | Lys | Gln | 145 | 150 | 155 | 160 |
| Leu | Ile | Asp | Lys | Leu | Glu | Glu | Arg | Phe | Arg | Phe | Asn | Arg | Lys | Asp | Leu | 165 | 170 | 175 |     |
| Ile | Gly | Phe | Glu | Phe | Thr | Val | Leu | Val | Ala | Leu | Glu | Leu | Ala | Leu | Tyr | 180 | 185 | 190 |     |
| Leu | Pro | Glu | Asn | Gln | Val | Leu | Pro | His | Tyr | Arg | Arg | Leu | Thr | Gln | Gln | 195 | 200 | 205 |     |

Phe

## (2) INFORMATION FOR SEQ ID NO:33:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

## (vii) IMMEDIATE SOURCE:

(B) CLONE: HW044

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 24..1100

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: complement (1161..1378)
- (D) OTHER INFORMATION: /label= SAC\_24216

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GTCGACCTCC ATAGAGTTCC GGC ATG AAG CCA CCG CAG AGA CGG CGG AAG   | 50  |
| Met Lys Pro Pro Gln Arg Arg Arg Lys                             |     |
| 1 5                                                             |     |
| GTC CCC GCA CGC TAC ACA GGT GAA GCT ACC GGC CCC ACA GCT TGG AGC | 98  |
| Val Pro Ala Arg Tyr Thr Gly Glu Ala Thr Gly Pro Thr Ala Trp Ser |     |
| 10 15 20 25                                                     |     |
| CCC CGC GAG ATG CGG CAC CTA CTG AGA CTA CTC CAG GCT CGG CGC GGC | 146 |
| Pro Arg Glu Met Arg His Leu Leu Arg Leu Leu Gln Ala Arg Arg Gly |     |
| 30 35 40                                                        |     |
| CAG CCG GAG CCA GAC GCC AAG GAG CTG GCC AAG GAG CTG CGA GGC CGG | 194 |
| Gln Pro Glu Pro Asp Ala Lys Glu Leu Ala Lys Glu Leu Arg Gly Arg |     |
| 45 50 55                                                        |     |
| AGC GAG GCC GAG ATC TGT CGC TTT ATC CAG CAG CTC AAA GGC CGG GTG | 242 |
| Ser Glu Ala Glu Ile Cys Arg Phe Ile Gln Gln Leu Lys Gly Arg Val |     |
| 60 65 70                                                        |     |
| GTT CGA GAG GCT ATT CGG AAG GTG CAA CCA GGT GGC AGA GAT GGT CCA | 290 |
| Val Arg Glu Ala Ile Arg Lys Val Gln Pro Gly Gly Arg Asp Gly Pro |     |
| 75 80 85                                                        |     |
| AGG CAT CGA GAG ACA CAG CTC CCA GCC CCC ATA GAG GTA TGG ATG GAT | 338 |
| Arg His Arg Glu Thr Gln Leu Pro Ala Pro Ile Glu Val Trp Met Asp |     |
| 90 95 100 105                                                   |     |
| CTT GCT GAG AAA TTA ACA GGC CCA CTG GAG GAA GCC CTG ACT GCA GCT | 386 |
| Leu Ala Glu Lys Leu Thr Gly Pro Leu Glu Glu Ala Leu Thr Ala Ala |     |
| 110 115 120                                                     |     |

|             |            |            |            |            |            |     |     |     |     |     |     |     |     |     |     |      |
|-------------|------------|------------|------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| TTC         | TCC        | CAG        | GTA        | CTC        | ACC        | ATT | GCT | GCT | GCG | GAA | CCT | CTC | AGC | CTC | CTG | 434  |
| Phe         | Ser        | Gln        | Val        | Leu        | Thr        | Ile | Ala | Ala | Ala | Glu | Pro | Leu | Ser | Leu | Leu |      |
|             |            | 125        |            |            |            |     |     | 130 |     |     |     |     | 135 |     |     |      |
| CAT         | TCC        | AAG        | CCA        | GGC        | AAG        | CCC | ACA | AAG | GCC | TGT | GGA | AGG | GCA | CTG | GTG | 482  |
| His         | Ser        | Lys        | Pro        | Gly        | Lys        | Pro | Thr | Lys | Ala | Cys | Gly | Arg | Ala | Leu | Val |      |
|             |            | 140        |            |            |            |     | 145 |     |     |     |     | 150 |     |     |     |      |
| TTC         | TTG        | AGC        | ACC        | CAA        | GAT        | GCG | CAG | AAG | GAT | TCT | GCC | CCT | GAA | GGT | TCT | 530  |
| Phe         | Leu        | Ser        | Thr        | Gln        | Asp        | Ala | Gln | Lys | Asp | Ser | Ala | Pro | Glu | Gly | Ser |      |
|             | 155        |            |            |            |            | 160 |     |     |     |     | 165 |     |     |     |     |      |
| GGG         | CCT        | GAA        | CCT        | ATG        | ACT        | GCT | GCT | GAC | CCC | ACT | CCT | GAG | GCC | TCT | GTC | 578  |
| Gly         | Pro        | Glu        | Pro        | Met        | Thr        | Ala | Ala | Asp | Pro | Thr | Pro | Glu | Ala | Ser | Val |      |
| 170         |            |            |            |            | 175        |     |     |     |     | 180 |     |     |     |     | 185 |      |
| CCT         | GAA        | CCT        | AAG        | GCC        | TCC        | GGT | ACC | AAC | CCT | GAG | ACC | TCT | GGC | CTT | GTC | 626  |
| Pro         | Glu        | Pro        | Lys        | Ala        | Ser        | Gly | Thr | Asn | Pro | Glu | Thr | Ser | Gly | Leu | Val |      |
|             |            |            |            | 190        |            |     |     |     | 195 |     |     |     |     | 200 |     |      |
| CCA         | GAG        | GTC        | TCT        | GTC        | CCT        | GAC | CCT | GAT | GCA | CCA | ACT | GAG | TCC | CTG | GCT | 674  |
| Pro         | Glu        | Val        | Ser        | Val        | Pro        | Asp | Pro | Asp | Ala | Pro | Thr | Glu | Ser | Leu | Ala |      |
|             |            |            | 205        |            |            |     |     | 210 |     |     |     |     | 215 |     |     |      |
| GGA         | TCC        | TCC        | ACA        | GAG        | AGA        | GAC | TTT | GCC | GTG | GAC | TTT | GAG | AAG | ATC | TAC | 722  |
| Gly         | Ser        | Ser        | Thr        | Glu        | Arg        | Asp | Phe | Ala | Val | Asp | Phe | Glu | Lys | Ile | Tyr |      |
|             |            | 220        |            |            |            |     | 225 |     |     |     |     | 230 |     |     |     |      |
| AAA         | TAC        | CTG        | TCC        | TCC        | TCC        | TCC | AGA | GGT | GGC | CAT | GGC | CCT | GAG | CTC | TCA | 770  |
| Lys         | Tyr        | Leu        | Ser        | Ser        | Ser        | Ser | Arg | Gly | Gly | His | Gly | Pro | Glu | Leu | Ser |      |
|             | 235        |            |            |            |            | 240 |     |     |     |     | 245 |     |     |     |     |      |
| GCA         | GTT        | GAG        | TCC        | GCC        | GTG        | GTC | CTT | AAC | CTG | CTC | ATG | TCA | CTT | GCA | GAG | 818  |
| Ala         | Val        | Glu        | Ser        | Ala        | Val        | Val | Leu | Asn | Leu | Leu | Met | Ser | Leu | Ala | Glu |      |
| 250         |            |            |            |            | 255        |     |     |     |     | 260 |     |     |     |     | 265 |      |
| GAA         | CTG        | CCC        | CAC        | CTG        | CCT        | TGC | ACA | GCC | CTG | GTG | GAC | CAT | CTG | ACT | AAA | 866  |
| Glu         | Leu        | Pro        | His        | Leu        | Pro        | Cys | Thr | Ala | Leu | Val | Asp | His | Leu | Thr | Lys |      |
|             |            |            |            | 270        |            |     |     |     | 275 |     |     |     |     | 280 |     |      |
| ACA         | TAT        | GCT        | CAA        | CTG        | ACG        | GCT | CCC | CAG | GCC | TCT | CTC | GAT | AGA | GAA | AAG | 914  |
| Thr         | Tyr        | Ala        | Gln        | Leu        | Thr        | Ala | Pro | Gln | Ala | Ser | Leu | Asp | Arg | Glu | Lys |      |
|             |            |            | 285        |            |            |     |     | 290 |     |     |     |     | 295 |     |     |      |
| AGG         | CCC        | AGG        | CCG        | GGG        | ACT        | GAA | GAT | GGA | GGG | ACT | GAC | TCC | ACG | GGG | CCA | 962  |
| Arg         | Pro        | Arg        | Pro        | Gly        | Thr        | Glu | Asp | Gly | Gly | Thr | Asp | Ser | Thr | Gly | Pro |      |
|             |            | 300        |            |            |            |     | 305 |     |     |     |     | 310 |     |     |     |      |
| GAA         | GAG        | ACT        | GGC        | CAA        | GGC        | AGT | CCT | CAA | GCT | TCT | GAG | CCC | ACA | GAA | CCG | 1010 |
| Glu         | Glu        | Thr        | Gly        | Gln        | Gly        | Ser | Pro | Gln | Ala | Ser | Glu | Pro | Thr | Glu | Pro |      |
|             | 315        |            |            |            |            | 320 |     |     |     |     | 325 |     |     |     |     |      |
| AGG         | CTG        | ACC        | TGG        | AAA        | GCA        | GCT | GGG | GTC | TGC | CCA | CTG | AAC | CCA | TTC | CTG | 1058 |
| Arg         | Leu        | Thr        | Trp        | Lys        | Ala        | Ala | Gly | Val | Cys | Pro | Leu | Asn | Pro | Phe | Leu |      |
| 330         |            |            |            |            | 335        |     |     |     |     | 340 |     |     |     |     | 345 |      |
| GTG         | CCC        | CTG        | GAC        | CTC        | CTG        | AGC | CAG | GCC | CTC | GCC | CCT | GCC | AGG |     |     | 1100 |
| Val         | Pro        | Leu        | Asp        | Leu        | Leu        | Ser | Gln | Ala | Leu | Ala | Pro | Ala | Arg |     |     |      |
|             |            |            |            | 350        |            |     |     |     | 355 |     |     |     |     |     |     |      |
| TGAAGGATGC  | AGCAGGCTGG | CTATGCTGGT | TTCTTTCTAC | ATCGTCTGTC | CAGCACTGGT |     |     |     |     |     |     |     |     |     |     | 1160 |
| ACTGGTGTCTG | GGAACGTGAT | TGTGGCTTCC | TGACAGTGTC | CGGCCATAGG | CAAGCCCTTC |     |     |     |     |     |     |     |     |     |     | 1220 |



AGACACTGCA TGCACTAGTA GCCTGGAAG TGAAGCACAG TTGAAGGAAG GGGTTTAACT 1280  
 ATTGGGGATT TGAGACTGCA CAAAGGCGGA ATTCCTGGGC TGGTAGATTG CGGCAAGTGT 1340  
 CCCTGGCCCC GCTGTGCCTG GTTCTCTGCC ATAAGAGTAC CACATCATCA TCCCTTTGTG 1400  
 CATGGCACTC GAACCCACCC CCAGCACACC CTCCCCACCT CAACTGACCA CTGTACCATC 1460  
 CTCTTCGCCC TTCTCTGGGT GTCCTGTGAC CCTCAATAAA GCTGTCATCT AACTAGCTGT 1520  
 GAAAAAAAAA AAGTCGAC 1538

## (2) INFORMATION FOR SEQ ID NO:34:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Lys Pro Pro Gln Arg Arg Arg Lys Val Pro Ala Arg Tyr Thr Gly  
 1 5 10 15  
 Glu Ala Thr Gly Pro Thr Ala Trp Ser Pro Arg Glu Met Arg His Leu  
 20 25 30  
 Leu Arg Leu Leu Gln Ala Arg Arg Gly Gln Pro Glu Pro Asp Ala Lys  
 35 40 45  
 Glu Leu Ala Lys Glu Leu Arg Gly Arg Ser Glu Ala Glu Ile Cys Arg  
 50 55 60  
 Phe Ile Gln Gln Leu Lys Gly Arg Val Val Arg Glu Ala Ile Arg Lys  
 65 70 75 80  
 Val Gln Pro Gly Gly Arg Asp Gly Pro Arg His Arg Glu Thr Gln Leu  
 85 90 95  
 Pro Ala Pro Ile Glu Val Trp Met Asp Leu Ala Glu Lys Leu Thr Gly  
 100 105 110  
 Pro Leu Glu Glu Ala Leu Thr Ala Ala Phe Ser Gln Val Leu Thr Ile  
 115 120 125  
 Ala Ala Ala Glu Pro Leu Ser Leu Leu His Ser Lys Pro Gly Lys Pro  
 130 135 140  
 Thr Lys Ala Cys Gly Arg Ala Leu Val Phe Leu Ser Thr Gln Asp Ala  
 145 150 155 160  
 Gln Lys Asp Ser Ala Pro Glu Gly Ser Gly Pro Glu Pro Met Thr Ala  
 165 170 175  
 Ala Asp Pro Thr Pro Glu Ala Ser Val Pro Glu Pro Lys Ala Ser Gly  
 180 185 190  
 Thr Asn Pro Glu Thr Ser Gly Leu Val Pro Glu Val Ser Val Pro Asp  
 195 200 205

Pro Asp Ala Pro Thr Glu Ser Leu Ala Gly Ser Ser Thr Glu Arg Asp  
 210 215 220  
 Phe Ala Val Asp Phe Glu Lys Ile Tyr Lys Tyr Leu Ser Ser Ser Ser  
 225 230 235 240  
 Arg Gly Gly His Gly Pro Glu Leu Ser Ala Val Glu Ser Ala Val Val  
 245 250 255  
 Leu Asn Leu Leu Met Ser Leu Ala Glu Glu Leu Pro His Leu Pro Cys  
 260 265 270  
 Thr Ala Leu Val Asp His Leu Thr Lys Thr Tyr Ala Gln Leu Thr Ala  
 275 280 285  
 Pro Gln Ala Ser Leu Asp Arg Glu Lys Arg Pro Arg Pro Gly Thr Glu  
 290 295 300  
 Asp Gly Gly Thr Asp Ser Thr Gly Pro Glu Glu Thr Gly Gln Gly Ser  
 305 310 315 320  
 Pro Gln Ala Ser Glu Pro Thr Glu Pro Arg Leu Thr Trp Lys Ala Ala  
 325 330 335  
 Gly Val Cys Pro Leu Asn Pro Phe Leu Val Pro Leu Asp Leu Leu Ser  
 340 345 350  
 Gln Ala Leu Ala Pro Ala Arg  
 355

## (2) INFORMATION FOR SEQ ID NO:35:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: HW045

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 9..1628

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1973..2134
- (D) OTHER INFORMATION: /label= SAC\_24028

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GTCGACCA GGG CGT GAT GGC TCC TAC TAC CAG CTC TTT GTT CAT GGT GGC  
 Gly Arg Asp Gly Ser Tyr Tyr Gln Leu Phe Val His Gly Gly  
 1 5 10

50

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| CGC | CTC | CAG | CCA | GTC | CTA | AGG | CAG | AAA | GCC | TGC | CGA | GGC | ATG | AAC | TGG | 98  |
| Arg | Leu | Gln | Pro | Val | Leu | Arg | Gln | Lys | Ala | Cys | Arg | Gly | Met | Asn | Trp |     |
| 15  |     |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |
| ATA | GCT | GGG | CTT | CGG | ATG | GTG | CCC | GAT | GGC | AGT | ATG | GTC | GTC | TTG | GGT | 146 |
| Ile | Ala | Gly | Leu | Arg | Met | Val | Pro | Asp | Gly | Ser | Met | Val | Val | Leu | Gly |     |
|     |     |     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |
| TTC | CAT | GCC | AAC | GAG | TTT | GTA | GTG | TGG | AGC | CCG | CGG | TCC | CAT | GAG | AAG | 194 |
| Phe | His | Ala | Asn | Glu | Phe | Val | Val | Trp | Ser | Pro | Arg | Ser | His | Glu | Lys |     |
|     |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| CTG | CAC | ATC | GTC | AAC | TGC | GGG | GGA | GGG | CAC | CGC | TCC | TGG | GCC | TTT | TCT | 242 |
| Leu | His | Ile | Val | Asn | Cys | Gly | Gly | Gly | His | Arg | Ser | Trp | Ala | Phe | Ser |     |
|     |     | 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     |
| GAT | ACT | GAG | GCA | GCC | ATG | GCC | TTT | GCC | TAC | CTT | AAG | GAT | GGT | GAT | GTC | 290 |
| Asp | Thr | Glu | Ala | Ala | Met | Ala | Phe | Ala | Tyr | Leu | Lys | Asp | Gly | Asp | Val |     |
|     | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |
| ATG | CTC | TAC | CGG | GCT | CTA | GGA | GGC | TGC | ATC | AGG | CCA | AAC | GTG | ATT | CTC | 338 |
| Met | Leu | Tyr | Arg | Ala | Leu | Gly | Gly | Cys | Ile | Arg | Pro | Asn | Val | Ile | Leu |     |
|     | 95  |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |
| CGG | GAG | GGT | CTG | CAT | GGC | CGG | GAA | ATC | ACA | TGT | GTA | AAG | CGT | GTG | GGC | 386 |
| Arg | Glu | Gly | Leu | His | Gly | Arg | Glu | Ile | Thr | Cys | Val | Lys | Arg | Val | Gly |     |
|     |     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |
| ACT | GTT | ACC | CTG | GGC | CCT | GAA | TTT | GAG | GTA | CCC | AAC | TTG | GAG | CAT | CCT | 434 |
| Thr | Val | Thr | Leu | Gly | Pro | Glu | Phe | Glu | Val | Pro | Asn | Leu | Glu | His | Pro |     |
|     |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| GAC | TCC | CTG | GAG | CCT | GGC | AGT | GAG | GGG | CCT | GGT | CTG | ATT | GAC | ATC | GTG | 482 |
| Asp | Ser | Leu | Glu | Pro | Gly | Ser | Glu | Gly | Pro | Gly | Leu | Ile | Asp | Ile | Val |     |
|     |     | 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |
| ATA | ACA | GGC | AGT | GAG | GAC | ACT | ACT | GTC | TGT | GTG | CTA | GCA | CTT | CCC | ACC | 530 |
| Ile | Thr | Gly | Ser | Glu | Asp | Thr | Thr | Val | Cys | Val | Leu | Ala | Leu | Pro | Thr |     |
|     | 160 |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     |
| ACC | ACA | GGC | GCA | GCC | CAC | GCC | CTC | ACT | GCT | GTC | TGT | AAC | CAT | ATC | TCC | 578 |
| Thr | Thr | Gly | Ala | Ala | His | Ala | Leu | Thr | Ala | Val | Cys | Asn | His | Ile | Ser |     |
|     | 175 |     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |
| TCC | GTG | CGA | GCC | CTG | GCA | GTG | TGG | GGT | GTT | GGC | ACC | CCA | GGT | GGC | CCA | 626 |
| Ser | Val | Arg | Ala | Leu | Ala | Val | Trp | Gly | Val | Gly | Thr | Pro | Gly | Gly | Pro |     |
|     |     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| CAG | GAT | TCT | CAC | CCA | GGG | CTC | ACG | GCT | CAG | GTA | GTG | TCT | GCA | GGG | GGT | 674 |
| Gln | Asp | Ser | His | Pro | Gly | Leu | Thr | Ala | Gln | Val | Val | Ser | Ala | Gly | Gly |     |
|     |     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |
| CGA | GCC | GAG | ATG | CAC | TGC | TTC | AGC | CTC | ATG | ATC | ACT | CCG | GAT | GCC | AGC | 722 |
| Arg | Ala | Glu | Met | His | Cys | Phe | Ser | Leu | Met | Ile | Thr | Pro | Asp | Ala | Ser |     |
|     |     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     |
| ACC | CCA | AGC | CGC | CTT | GCC | TGC | CAC | ATC | ATG | CAC | CTT | TCA | TCC | CAC | CGG | 770 |
| Thr | Pro | Ser | Arg | Leu | Ala | Cys | His | Ile | Met | His | Leu | Ser | Ser | His | Arg |     |
|     | 240 |     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |     |
| CTA | GAT | GAG | TAC | TGG | GAC | CGG | CAG | CGC | AAC | CGG | CAC | CGG | ATG | ATC | AAG | 818 |
| Leu | Asp | Glu | Tyr | Trp | Asp | Arg | Gln | Arg | Asn | Arg | His | Arg | Met | Ile | Lys |     |
|     | 255 |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| GTG | GAC | CCT | GAG | ACC | AGG | TAC | ATG | TCT | CTT | GCC | ATT | TGT | GAG | CTT | GAC | 866  |
| Val | Asp | Pro | Glu | Thr | Arg | Tyr | Met | Ser | Leu | Ala | Ile | Cys | Glu | Leu | Asp |      |
|     |     |     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |      |
| TCC | GAT | AGG | CCT | GGC | CTT | GGC | CCC | GGC | CCC | CTT | GTG | GCT | GCA | GCC | TGT | 914  |
| Ser | Asp | Arg | Pro | Gly | Leu | Gly | Pro | Gly | Pro | Leu | Val | Ala | Ala | Ala | Cys |      |
|     |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |      |
| AGT | GAC | GGG | GCA | GTG | AGG | CTT | TTT | CTC | TTG | CAG | GAC | TCT | GGG | CGA | ATT | 962  |
| Ser | Asp | Gly | Ala | Val | Arg | Leu | Phe | Leu | Leu | Gln | Asp | Ser | Gly | Arg | Ile |      |
|     |     | 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |      |
| CTG | CAT | CTC | CTT | GCT | GAG | ACT | TTC | CAC | CAT | AAG | CGG | TGT | GTC | CTC | AAG | 1010 |
| Leu | His | Leu | Leu | Ala | Glu | Thr | Phe | His | His | Lys | Arg | Cys | Val | Leu | Lys |      |
|     |     | 320 |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |      |
| GTC | CAT | TCG | TTC | ACA | CAT | GAG | GCA | CCC | AAC | CAG | CGT | CGG | AGG | CTG | ATC | 1058 |
| Val | His | Ser | Phe | Thr | His | Glu | Ala | Pro | Asn | Gln | Arg | Arg | Arg | Leu | Ile |      |
|     |     |     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |      |
| CTG | TGC | AGT | GCA | GCT | ACA | GAT | GGC | AGC | ATA | GCC | TTC | TGG | GAT | CTC | ACC | 1106 |
| Leu | Cys | Ser | Ala | Ala | Thr | Asp | Gly | Ser | Ile | Ala | Phe | Trp | Asp | Leu | Thr |      |
|     |     |     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |      |
| ACG | GCA | ATG | GAC | CGA | GGC | TCT | ACT | ACC | CTG | GAG | CCT | CCA | GCA | CAC | CCT | 1154 |
| Thr | Ala | Met | Asp | Arg | Gly | Ser | Thr | Thr | Leu | Glu | Pro | Pro | Ala | His | Pro |      |
|     |     |     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |      |
| GGG | CTT | CCC | TAC | CAG | ATG | GGC | ACC | CCC | TGC | CTG | ACC | GTC | CAG | GCC | CAT | 1202 |
| Gly | Leu | Pro | Tyr | Gln | Met | Gly | Thr | Pro | Cys | Leu | Thr | Val | Gln | Ala | His |      |
|     |     | 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |      |
| AGC | TGT | GGT | GTC | AAC | AGC | CTG | CAC | ACT | TTG | CCT | ACA | CCT | GAG | GGC | CAT | 1250 |
| Ser | Cys | Gly | Val | Asn | Ser | Leu | His | Thr | Leu | Pro | Thr | Pro | Glu | Gly | His |      |
|     | 400 |     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     |      |
| CAT | CTT | GTG | GCC | AGT | GGC | AGT | GAG | GAC | GGG | TCC | CTG | CAT | GTC | TTC | ACG | 1298 |
| His | Leu | Val | Ala | Ser | Gly | Ser | Glu | Asp | Gly | Ser | Leu | His | Val | Phe | Thr |      |
|     |     |     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |      |
| CTT | GCT | GTG | AAG | ATG | CCA | GAG | CTG | GAA | GAG | GCT | GAT | GGG | GAG | GCT | GAG | 1346 |
| Leu | Ala | Val | Lys | Met | Pro | Glu | Leu | Glu | Glu | Ala | Asp | Gly | Glu | Ala | Glu |      |
|     |     |     |     | 435 |     |     |     |     | 440 |     |     |     |     | 445 |     |      |
| TTG | GTG | CCC | CAG | TTA | TGT | GTC | CTA | GAT | GAA | TAT | TCT | GTC | CCC | TGT | GCA | 1394 |
| Leu | Val | Pro | Gln | Leu | Cys | Val | Leu | Asp | Glu | Tyr | Ser | Val | Pro | Cys | Ala |      |
|     |     |     | 450 |     |     |     |     | 455 |     |     |     |     | 460 |     |     |      |
| CAT | GCT | GCC | CAT | GTG | ACG | GGC | ATC | AAG | ATC | CTA | AGT | CCC | AAG | CTG | ATG | 1442 |
| His | Ala | Ala | His | Val | Thr | Gly | Ile | Lys | Ile | Leu | Ser | Pro | Lys | Leu | Met |      |
|     |     | 465 |     |     |     |     | 470 |     |     |     |     | 475 |     |     |     |      |
| GTC | TCA | GCC | TCC | ATA | GAC | CAA | CGG | CTG | ACC | TTC | TGG | CGT | CTT | GGA | AAT | 1490 |
| Val | Ser | Ala | Ser | Ile | Asp | Gln | Arg | Leu | Thr | Phe | Trp | Arg | Leu | Gly | Asn |      |
|     |     | 480 |     |     |     |     | 485 |     |     |     | 490 |     |     |     |     |      |
| GGT | GAG | CCC | ACC | TTC | ATG | AAT | AGC | ACT | GTG | TAC | CAC | GTG | CCA | GAT | GTG | 1538 |
| Gly | Glu | Pro | Thr | Phe | Met | Asn | Ser | Thr | Val | Tyr | His | Val | Pro | Asp | Val |      |
|     |     |     |     |     | 500 |     |     |     |     | 505 |     |     |     |     | 510 |      |
| GCT | GAC | ATG | GAC | TGC | TGG | CCT | GTG | AAC | CCT | GAG | TTT | GGC | CAC | CGC | TGT | 1586 |
| Ala | Asp | Met | Asp | Cys | Trp | Pro | Val | Asn | Pro | Glu | Phe | Gly | His | Arg | Cys |      |

| 515                                                                | 520 | 525 |      |
|--------------------------------------------------------------------|-----|-----|------|
| GCT CTT GCG GGT CAG GGA CTC GAG GTT TAC AAC TGG TAT GAC            |     |     | 1628 |
| Ala Leu Ala Gly Gln Gly Leu Glu Val Tyr Asn Trp Tyr Asp            |     |     |      |
| 530                                                                | 535 | 540 |      |
| TGAGTTACCA CAGTAGTTGG AGGACTGAGC CTGGGGCTTG ACCACAGACA GCGGAGCAGG  |     |     | 1688 |
| GATCAGCTGT CTGTGTCATG CTCTATGTGC TCTGAGGAGG TGAGGCAGTA CCATGGGTTC  |     |     | 1748 |
| CTGTAGGGTG TTGCATAGGT GGACCAAGAA TATGCCTCAC TCTTCACAAT AGGATGAAAC  |     |     | 1808 |
| TGTATTTATT CTGACTTTAA GTGCCCAACA TCTGTGAGGT TTCTGTGAGG TCTTGTTTTT  |     |     | 1868 |
| TTCCCAAGTTG ATGCTTTTAT AAACATTCCC AGCTATTGGG CCCTTAGATG TGGCTCAGCG |     |     | 1928 |
| GAGGGAGGCC CAGCATGGCC AAGCCTGTGT GGAACACCTC ACGTACTGCC CTCAAAAGCT  |     |     | 1988 |
| GTAGGCGAGC AAACATCTGA CCAAAGAGGT GTGGCCGAGG TTCCTGAAAG AAAAGCAACC  |     |     | 2048 |
| AGGCCCATCC TCATTTCCTG AGCCTGAGCC CTTGTCCATA TTTCCACAG ACCCTCCCTT   |     |     | 2108 |
| GCTGTATGCT CACCCCTAGA ATGTGTACGC GGTATAGTA TGAGCTGAAA TCCATGCTGA   |     |     | 2168 |
| GCTGCACCAG GAACTGACAC ACCTAGAGAC AGAGGTTGGA TCGTTGAGCT GTTGTCTTTT  |     |     | 2228 |
| TTCTTGTGTC ACAACCCAGA ATAAAGAATA GTGTGTGTAG TGTCAAAAA              |     |     | 2277 |

## (2) INFORMATION FOR SEQ ID NO:36:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Gly Arg Asp Gly Ser Tyr Tyr Gln Leu Phe Val His Gly Gly Arg Leu |  |
| 1 5 10 15                                                       |  |
| Gln Pro Val Leu Arg Gln Lys Ala Cys Arg Gly Met Asn Trp Ile Ala |  |
| 20 25 30                                                        |  |
| Gly Leu Arg Met Val Pro Asp Gly Ser Met Val Val Leu Gly Phe His |  |
| 35 40 45                                                        |  |
| Ala Asn Glu Phe Val Val Trp Ser Pro Arg Ser His Glu Lys Leu His |  |
| 50 55 60                                                        |  |
| Ile Val Asn Cys Gly Gly Gly His Arg Ser Trp Ala Phe Ser Asp Thr |  |
| 65 70 75 80                                                     |  |
| Glu Ala Ala Met Ala Phe Ala Tyr Leu Lys Asp Gly Asp Val Met Leu |  |
| 85 90 95                                                        |  |
| Tyr Arg Ala Leu Gly Gly Cys Ile Arg Pro Asn Val Ile Leu Arg Glu |  |
| 100 105 110                                                     |  |
| Gly Leu His Gly Arg Glu Ile Thr Cys Val Lys Arg Val Gly Thr Val |  |
| 115 120 125                                                     |  |

Thr Leu Gly Pro Glu Phe Glu Val Pro Asn Leu Glu His Pro Asp Ser  
 130 135 140  
 Leu Glu Pro Gly Ser Glu Gly Pro Gly Leu Ile Asp Ile Val Ile Thr  
 145 150 155 160  
 Gly Ser Glu Asp Thr Thr Val Cys Val Leu Ala Leu Pro Thr Thr Thr  
 165 170 175  
 Gly Ala Ala His Ala Leu Thr Ala Val Cys Asn His Ile Ser Ser Val  
 180 185 190  
 Arg Ala Leu Ala Val Trp Gly Val Gly Thr Pro Gly Gly Pro Gln Asp  
 195 200 205  
 Ser His Pro Gly Leu Thr Ala Gln Val Val Ser Ala Gly Gly Arg Ala  
 210 215 220  
 Glu Met His Cys Phe Ser Leu Met Ile Thr Pro Asp Ala Ser Thr Pro  
 225 230 235 240  
 Ser Arg Leu Ala Cys His Ile Met His Leu Ser Ser His Arg Leu Asp  
 245 250 255  
 Glu Tyr Trp Asp Arg Gln Arg Asn Arg His Arg Met Ile Lys Val Asp  
 260 265 270  
 Pro Glu Thr Arg Tyr Met Ser Leu Ala Ile Cys Glu Leu Asp Ser Asp  
 275 280 285  
 Arg Pro Gly Leu Gly Pro Gly Pro Leu Val Ala Ala Ala Cys Ser Asp  
 290 295 300  
 Gly Ala Val Arg Leu Phe Leu Leu Gln Asp Ser Gly Arg Ile Leu His  
 305 310 315 320  
 Leu Leu Ala Glu Thr Phe His His Lys Arg Cys Val Leu Lys Val His  
 325 330 335  
 Ser Phe Thr His Glu Ala Pro Asn Gln Arg Arg Arg Leu Ile Leu Cys  
 340 345 350  
 Ser Ala Ala Thr Asp Gly Ser Ile Ala Phe Trp Asp Leu Thr Thr Ala  
 355 360 365  
 Met Asp Arg Gly Ser Thr Thr Leu Glu Pro Pro Ala His Pro Gly Leu  
 370 375 380  
 Pro Tyr Gln Met Gly Thr Pro Cys Leu Thr Val Gln Ala His Ser Cys  
 385 390 395 400  
 Gly Val Asn Ser Leu His Thr Leu Pro Thr Pro Glu Gly His His Leu  
 405 410 415  
 Val Ala Ser Gly Ser Glu Asp Gly Ser Leu His Val Phe Thr Leu Ala  
 420 425 430  
 Val Lys Met Pro Glu Leu Glu Glu Ala Asp Gly Glu Ala Glu Leu Val  
 435 440 445  
 Pro Gln Leu Cys Val Leu Asp Glu Tyr Ser Val Pro Cys Ala His Ala  
 450 455 460

Ala His Val Thr Gly Ile Lys Ile Leu Ser Pro Lys Leu Met Val Ser  
 465 470 475 480

Ala Ser Ile Asp Gln Arg Leu Thr Phe Trp Arg Leu Gly Asn Gly Glu  
 485 490 495

Pro Thr Phe Met Asn Ser Thr Val Tyr His Val Pro Asp Val Ala Asp  
 500 505 510

Met Asp Cys Trp Pro Val Asn Pro Glu Phe Gly His Arg Cys Ala Leu  
 515 520 525

Ala Gly Gln Gly Leu Glu Val Tyr Asn Trp Tyr Asp  
 530 535 540

## (2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2373 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: HW046

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 9..1160

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: complement (1523..1760)  
 (D) OTHER INFORMATION: /label= SAC\_24036

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

|                                                                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GTCTGACGT                                                       | GAC | TTC | CTT | GTC | AGG | TTC | ACC | CCC | GCT | GCA | GCA | GGG | CTC | TGC | 50  |
|                                                                 | Asp | Phe | Leu | Val | Arg | Phe | Thr | Pro | Ala | Ala | Ala | Gly | Leu | Cys |     |
|                                                                 | 1   |     |     |     | 5   |     |     |     |     |     |     |     |     | 10  |     |
| TCT CTG ACT GAG TGG TGC TGT GTT ACA TGG ATC TGT CAT TTC TAT TCA |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 98  |
| Ser Leu Thr Glu Trp Cys Cys Val Thr Trp Ile Cys His Phe Tyr Ser |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| 15                                                              |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| GTC ATC AGT TGG CAT TGC AGT AAC ACC TAT GGC AAT GAA GAA AGA GAC |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 146 |
| Val Ile Ser Trp His Cys Ser Asn Thr Tyr Gly Asn Glu Glu Arg Asp |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|                                                                 |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |
| AGA ATT TGG GAT TTT CAT CTA AGG AAA ATG ATA AAT AAC AAC CAG ACG |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 194 |
| Arg Ile Trp Asp Phe His Leu Arg Lys Met Ile Asn Asn Asn Gln Thr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|                                                                 |     |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |
| TGT GCT GCA GGG CAG GAC TCC GTG CCC TAC GTG ACC TGT ATG CTT CAC |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 242 |
| Cys Ala Ala Gly Gln Asp Ser Val Pro Tyr Val Thr Cys Met Leu His |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|                                                                 |     |     |     | 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |

|                                                                                                                                                       |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| GTG CTG GAA GAG TGG TTG GGT GTG GAA CAG TTG GAG GAC TAC CTG AAT<br>Val Leu Glu Glu Trp Leu Gly Val Glu Gln Leu Glu Asp Tyr Leu Asn<br>80 85 90        | 290 |
| TTT GCG AAC CAT CTC TTG TGG GTC TTC ACC CCG CTG ATC CTT TTA ATA<br>Phe Ala Asn His Leu Leu Trp Val Phe Thr Pro Leu Ile Leu Leu Ile<br>95 100 105 110  | 338 |
| CTT CCG TAC TTT ACC ATC TTC CTT CTC TAC CTT ACT ATT ATT TTC CTC<br>Leu Pro Tyr Phe Thr Ile Phe Leu Leu Tyr Leu Thr Ile Ile Phe Leu<br>115 120 125     | 386 |
| CAC ATC TAT AAG AGG AAG AAT GTG TTA AAA GAA GCC TAC TCT CAC AAC<br>His Ile Tyr Lys Arg Lys Asn Val Leu Lys Glu Ala Tyr Ser His Asn<br>130 135 140     | 434 |
| TTG TGG GAT GGC GCG AGG AAA ACA GTG GCA ACC CTG TGG GAT GGA CAT<br>Leu Trp Asp Gly Ala Arg Lys Thr Val Ala Thr Leu Trp Asp Gly His<br>145 150 155     | 482 |
| GCG GCG GTT TGG CAT GGT TAT GAA GTT CAC GGG ATG GAA AAG ATA CCA<br>Ala Ala Val Trp His Gly Tyr Glu Val His Gly Met Glu Lys Ile Pro<br>160 165 170     | 530 |
| GAA GGA CCA GCA CTT ATA ATT TTT TAT CAT GGA GCT ATT CCC ATA GAC<br>Glu Gly Pro Ala Leu Ile Ile Phe Tyr His Gly Ala Ile Pro Ile Asp<br>175 180 185 190 | 578 |
| TTT TAC TAC TTC ATG GCT AAA ATT TTC ATC CAC AAA GGC AGA ACT TGC<br>Phe Tyr Tyr Phe Met Ala Lys Ile Phe Ile His Lys Gly Arg Thr Cys<br>195 200 205     | 626 |
| CGA GTG GTA GCT GAC CAC TTT GTC TTT AAA ATC CCA GGG TTC AGT TTA<br>Arg Val Val Ala Asp His Phe Val Phe Lys Ile Pro Gly Phe Ser Leu<br>210 215 220     | 674 |
| TTA CTT GAT GTA TTT TGT GCT CTT CAT GGA CCA AGA GAA AAA TGT GTT<br>Leu Leu Asp Val Phe Cys Ala Leu His Gly Pro Arg Glu Lys Cys Val<br>225 230 235     | 722 |
| GAA ATC TTG AGG AGT GGT CAC TTG TTA GCT ATT TCA CCG GGT GGA GTT<br>Glu Ile Leu Arg Ser Gly His Leu Leu Ala Ile Ser Pro Gly Gly Val<br>240 245 250     | 770 |
| CGA GAA GCC TTA CTT AGT GAT GAA ACC TAC AAC ATC ATA TGG GGT AAT<br>Arg Glu Ala Leu Leu Ser Asp Glu Thr Tyr Asn Ile Ile Trp Gly Asn<br>255 260 265 270 | 818 |
| CGT AAA GGC TTT GCT CAG GTT GCA ATC GAT GCA AAA GTG CCC ATT ATT<br>Arg Lys Gly Phe Ala Gln Val Ala Ile Asp Ala Lys Val Pro Ile Ile<br>275 280 285     | 866 |
| CCT ATG TTT ACA CAA AAC ATC CGA GAA GGA TTT AGA TCA CTC GGA GGA<br>Pro Met Phe Thr Gln Asn Ile Arg Glu Gly Phe Arg Ser Leu Gly Gly<br>290 295 300     | 914 |
| ACA AGA TTG TTT AAA TGG CTT TAT GAA AAA TTC CGC TAT CCG TTT GCT<br>Thr Arg Leu Phe Lys Trp Leu Tyr Glu Lys Phe Arg Tyr Pro Phe Ala<br>305 310 315     | 962 |
| CCA ATG TAT GGA GGT TTT CCT GTG AAG TTG CGG ACC TTC TTG GGT GAT<br>Pro Met Tyr Gly Gly Phe Pro Val Lys Leu Arg Thr Phe Leu Gly Asp<br>1010            |     |



| 320                                                                                                                                               | 325                                               | 330                                                           |      |
|---------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------|---------------------------------------------------------------|------|
| CCT ATT CCG TAT GAC<br>Pro Ile Pro Tyr Asp<br>335                                                                                                 | CCA GAG GTA ACA GCA<br>Pro Glu Val Thr Ala<br>340 | GAA GAA TTA GCT GAA AAG<br>Glu Glu Leu Ala Glu Lys<br>345 350 | 1058 |
| ACT AAG AAC GCT GTT CAA GCT TTG ATC GAC AAG CAC CAA AGG ATA CCG<br>Thr Lys Asn Ala Val Gln Ala Leu Ile Asp Lys His Gln Arg Ile Pro<br>355 360 365 |                                                   |                                                               | 1106 |
| GGG AAC ATT AGG AGT GCT TTG CTG GAC CGC TTT CAT AAA GAG CAG AAG<br>Gly Asn Ile Arg Ser Ala Leu Leu Asp Arg Phe His Lys Glu Gln Lys<br>370 375 380 |                                                   |                                                               | 1154 |
| GCT AAT TGACAGATAA TTTCGTGTGT CTCTAATGCC AAGTTTGCAT CTGTGGTACT<br>Ala Asn                                                                         |                                                   |                                                               | 1210 |
| GCCTTTTAAA CTTTGTAGG TTGTATAATA GTCTTTTAA AACCTGCTAA TGAGCATCTT                                                                                   |                                                   |                                                               | 1270 |
| TCTTTAGAAT TTAAACTTTC TATGGTTAAT CTTACCCCTT CAATCAGTTT TGTCAAATGT                                                                                 |                                                   |                                                               | 1330 |
| AGTAAGTAAC TCACCATTTG CTTGACTCAG AAGATGATCA TGTTGCATTT GCAATCCTTA                                                                                 |                                                   |                                                               | 1390 |
| GTAGTATATG ATAGGCACAA GTCTTCCTGG ATAACAGCAG TCTAGGTTAG GCAGACTTCA                                                                                 |                                                   |                                                               | 1450 |
| CTAAATTATG CTTCTGTGTT TGTGTCTGTT GTGCCAATGG GATGGTGAGA GGTACCTGAG                                                                                 |                                                   |                                                               | 1510 |
| CTGGGGTGTA GCACTTGCTT AGTTTAGGTG AGCGGTGCCT TTGTATCCAT CCTTCATTCC                                                                                 |                                                   |                                                               | 1570 |
| ACTCACAACT GCTGGTAAGT TGTGGAACGC TTTTGCACCT CCGTGGTTTA TGTTAAGCAT                                                                                 |                                                   |                                                               | 1630 |
| GGTAATACTG TGGTGGTGAA CATTAAGTTG CTTATGTCTA CTGTGATATA TCCGTATCTA                                                                                 |                                                   |                                                               | 1690 |
| TATATCTGAT AGATATCTGT AGTGAGAAAT CTGTAATTGA ATTGATTCCT GAATCCTTTA                                                                                 |                                                   |                                                               | 1750 |
| GGAGTTATGT ACATTTTGT CCATTGGGTA TTGAAATTAC TCCTTCAGGG ATGATGTCCA                                                                                  |                                                   |                                                               | 1810 |
| GTGCCAAGC ACAATGAAAG AGATGTACTA TTTTGTAAAT CAAATCATTG TTACTTGTAG                                                                                  |                                                   |                                                               | 1870 |
| TATTTATTAA CAGAGTTGTT TGGTATTTAT TTTAAACAAG GATCTAAGTA AATGTATAGG                                                                                 |                                                   |                                                               | 1930 |
| ATGGATTGTC AGCACGTGTC TTACACGGTG TAAAGATAAA ATCGTGGGCA CGCTCTGCAG                                                                                 |                                                   |                                                               | 1990 |
| TTTATGTTAG AGCAGATCCT AGGCTGAGGA GTGACAACTG AGGAAGCTCT GCCTCGCTTA                                                                                 |                                                   |                                                               | 2050 |
| TCCCAGGGCT CGCTTCCGTG CTCTGCAGCC AGTCACGTGG TTATATCTGT AAAATGTACT                                                                                 |                                                   |                                                               | 2110 |
| TGAATGATGA ATTTCTGTAA ACATGGAGTC CTCTGAAAAT GTAATTACTT TGAATTGTTG                                                                                 |                                                   |                                                               | 2170 |
| TCTTCTTGAA AACTTATTTT AAAAGTATTT AAACAGCCAA GTATCATGAA TTCATCGCAG                                                                                 |                                                   |                                                               | 2230 |
| TGTGTCTTCC CCCTTTCAG TACTTGGGTT TTATATGGAC TTTTAACTA CAAGTGTATA                                                                                   |                                                   |                                                               | 2290 |
| TTTGTGATAT GTATAATGTA TGTATAATGT ATATAGAAAT GGTGTGAAAA TAAAGCTGAA                                                                                 |                                                   |                                                               | 2350 |
| CTGCAACTCC TCTCTAGTAA AAA                                                                                                                         |                                                   |                                                               | 2373 |

## (2) INFORMATION FOR SEQ ID NO:38:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 384 amino acids

(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

Asp Phe Leu Val Arg Phe Thr Pro Ala Ala Ala Gly Leu Cys Ser Leu
 1 5 10
Thr Glu Trp Cys Cys Val Thr Trp Ile Cys His Phe Tyr Ser Val Ile
 20 25 30
Ser Trp His Cys Ser Asn Thr Tyr Gly Asn Glu Glu Arg Asp Arg Ile
 35 40 45
Trp Asp Phe His Leu Arg Lys Met Ile Asn Asn Asn Gln Thr Cys Ala
 50 55 60
Ala Gly Gln Asp Ser Val Pro Tyr Val Thr Cys Met Leu His Val Leu
 65 70 75 80
Glu Glu Trp Leu Gly Val Glu Gln Leu Glu Asp Tyr Leu Asn Phe Ala
 85 90 95
Asn His Leu Leu Trp Val Phe Thr Pro Leu Ile Leu Leu Ile Leu Pro
 100 105 110
Tyr Phe Thr Ile Phe Leu Leu Tyr Leu Thr Ile Ile Phe Leu His Ile
 115 120 125
Tyr Lys Arg Lys Asn Val Leu Lys Glu Ala Tyr Ser His Asn Leu Trp
 130 135 140
Asp Gly Ala Arg Lys Thr Val Ala Thr Leu Trp Asp Gly His Ala Ala
 145 150 155 160
Val Trp His Gly Tyr Glu Val His Gly Met Glu Lys Ile Pro Glu Gly
 165 170 175
Pro Ala Leu Ile Ile Phe Tyr His Gly Ala Ile Pro Ile Asp Phe Tyr
 180 185 190
Tyr Phe Met Ala Lys Ile Phe Ile His Lys Gly Arg Thr Cys Arg Val
 195 200 205
Val Ala Asp His Phe Val Phe Lys Ile Pro Gly Phe Ser Leu Leu Leu
 210 215 220
Asp Val Phe Cys Ala Leu His Gly Pro Arg Glu Lys Cys Val Glu Ile
 225 230 235 240
Leu Arg Ser Gly His Leu Leu Ala Ile Ser Pro Gly Gly Val Arg Glu
 245 250 255
Ala Leu Leu Ser Asp Glu Thr Tyr Asn Ile Ile Trp Gly Asn Arg Lys
 260 265 270
Gly Phe Ala Gln Val Ala Ile Asp Ala Lys Val Pro Ile Ile Pro Met
 275 280 285
Phe Thr Gln Asn Ile Arg Glu Gly Phe Arg Ser Leu Gly Gly Thr Arg
 290 295 300

```

Leu Phe Lys Trp Leu Tyr Glu Lys Phe Arg Tyr Pro Phe Ala Pro Met  
 305 310 315 320  
 Tyr Gly Gly Phe Pro Val Lys Leu Arg Thr Phe Leu Gly Asp Pro Ile  
 325 330 335  
 Pro Tyr Asp Pro Glu Val Thr Ala Glu Glu Leu Ala Glu Lys Thr Lys  
 340 345 350  
 Asn Ala Val Gln Ala Leu Ile Asp Lys His Gln Arg Ile Pro Gly Asn  
 355 360 365  
 Ile Arg Ser Ala Leu Leu Asp Arg Phe His Lys Glu Gln Lys Ala Asn  
 370 375 380

## (2) INFORMATION FOR SEQ ID NO:39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: HW047

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 8..511

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: complement (1675..1833)
- (D) OTHER INFORMATION: /label= SAC\_23915

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

|                                                                 |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
|-----------------------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| GTCGACC                                                         | AGG | GCC | TTC | CAT | CAG | ACC | TGC | CCA | AAC | TTT | GTC | ATA | GAG | AAG | 49 |
|                                                                 | Arg | Ala | Phe | His | Gln | Thr | Cys | Pro | Asn | Phe | Val | Ile | Glu | Lys |    |
|                                                                 | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |    |
| ATT GAA AGG ATT CAA AAT CCA GCT CTT TGG AGG AGG TAC CAG GCG TAC | 97  |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Ile Glu Arg Ile Gln Asn Pro Ala Leu Trp Arg Arg Tyr Gln Ala Tyr |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| 15 20 25 30                                                     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| AAA AAA ATT ATG GAT GAA AAG AAT GGC AAT GTG ATA AAT GAG AAG CAA | 145 |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Lys Lys Ile Met Asp Glu Lys Asn Gly Asn Val Ile Asn Glu Lys Gln |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| 35 40 45                                                        |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| CTC TTC CAT GGG ACG GAG TTT GGC TCT CTG GCA CAG CTC AAC AGT AAT | 193 |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Leu Phe His Gly Thr Glu Phe Gly Ser Leu Ala Gln Leu Asn Ser Asn |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| 50 55 60                                                        |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| GGA TTT AAC CGC AGC TAT GCT GGG AAG AAC GCT ACG GCT TAT GGG AAA | 241 |     |     |     |     |     |     |     |     |     |     |     |     |     |    |
| Gly Phe Asn Arg Ser Tyr Ala Gly Lys Asn Ala Thr Ala Tyr Gly Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |     |    |

| 65                                                                                                                                                   | 70 | 75 |      |
|------------------------------------------------------------------------------------------------------------------------------------------------------|----|----|------|
| GGA ACC TAT TTT GCA GTC AAT GCT TCC TAT TCT GCC CAT GAC ACA TAT<br>Gly Thr Tyr Phe Ala Val Asn Ala Ser Tyr Ser Ala His Asp Thr Tyr<br>80 85 90       |    |    | 289  |
| TCC AAA CCA GAT GCC AAT GGG AAA AAG TAT ATG TAT TAT GTG CGG GTC<br>Ser Lys Pro Asp Ala Asn Gly Lys Lys Tyr Met Tyr Tyr Val Arg Val<br>95 100 105 110 |    |    | 337  |
| CTC ACT GGA AAC TAC ACA CAA GGA AAC GCA TCA CTG ATT GTG CCT CCT<br>Leu Thr Gly Asn Tyr Thr Gln Gly Asn Ala Ser Leu Ile Val Pro Pro<br>115 120 125    |    |    | 385  |
| TCA AGG GAC CCT CAA AAT GCT ACT GAC TTG TTT GAC ACT GTC GCA GAT<br>Ser Arg Asp Pro Gln Asn Ala Thr Asp Leu Phe Asp Thr Val Ala Asp<br>130 135 140    |    |    | 433  |
| AAT GTT ATA AAT CCG AGT ATA TTT GTA GTG TTT TAT GAC AAT CAA GCA<br>Asn Val Ile Asn Pro Ser Ile Phe Val Val Phe Tyr Asp Asn Gln Ala<br>145 150 155    |    |    | 481  |
| TAC CCT GAG TAT CTT ATC ACA TTT AGG AAG TAACACTTTG GGGTGCCTTC<br>Tyr Pro Glu Tyr Leu Ile Thr Phe Arg Lys<br>160 165                                  |    |    | 531  |
| TGAAAGACAT TGGTATCTGC CGTAGGACAA ATTTTAGCTG TTTTCCTTCT TAGACTTTCT                                                                                    |    |    | 591  |
| TCTCTAAGAG CACGAGGTCT TTCTCTGCCA CGGATTGTTT CCTCAGCTGC CCCTTCATAG                                                                                    |    |    | 651  |
| TGAACATGAA CCTACTTGAG GGCCAACCAC TTGAGAATTT CAAGCAGGTG ACAGCTTTAG                                                                                    |    |    | 711  |
| CTGCCTTCAC AAATGTGAAC CTCAAATCCA CGGAAAAGAA CAAACTTACG TTCTGGAAGG                                                                                    |    |    | 771  |
| ACAATAAAAC CTTTATGCAC TTTCAGAAAG CCCACAATAC ACCCACCACC AGTGGAGTTA                                                                                    |    |    | 831  |
| CATCAGAGCA CCACTGTGCT GAGGGGCACC CAGGACCACT GAGCCAGTAA GGCTGCCAAC                                                                                    |    |    | 891  |
| TGAACAGATT CCAAGACAGA GAACTTCGTT CATCACTAAC AGCGCCGTGT CCTGTGGGTT                                                                                    |    |    | 951  |
| GGACAGTTCC AGCCAGGGTT ATGTACAGAC TGGGTTCTGG GATGTGGCTC TGGGTCTGTG                                                                                    |    |    | 1011 |
| TGAACTGAGC CCCCCAAGGA GAGGCACAGC TGAAGCCCTG TCAGGGGGCC CTTTAAATGT                                                                                    |    |    | 1071 |
| TGACACCAAT GTTGAGGCTA CCTAGTGAAG AAATGGGATG GGGCCTGCTA CCTCTCCTGT                                                                                    |    |    | 1131 |
| GGAAGTCCTT CTACTGGGTG AAAATGAATG AACTCTAACA GTATTGGCTA GCGTCTTTCT                                                                                    |    |    | 1191 |
| TGTGGCAGGC TGGCTTGTGA TAACTTGAAG CTTTATGACT AAGTCAGTCA TTTTGCTAAC                                                                                    |    |    | 1251 |
| TCACTAACAG TATCTACTGG ATGCGATTG TTTCTTGTGA TGCCAGAGAT CACCCAGAGC                                                                                     |    |    | 1311 |
| CTCACATGGG CCAGGCAAGC ACTCTACTAC TGAACATAT TCCCAGCCTC TTAGTGAGGC                                                                                     |    |    | 1371 |
| AAGACTCCAC TAAGTTGCCC TGGCAGGTTT GAACTCATTA TCTTCCTGCA TTGGCTACTT                                                                                    |    |    | 1431 |
| ATTGGGGTGG GGTGGGGTGC TTAAATGTGT CTTTAAATTT TCTCCTGTAC TCCCATTAT                                                                                     |    |    | 1491 |
| TGAGTGCCTG GACCCTTGTC AGGTAGAATA AGAGGTGTGT TCACATAGAT AATTTTGTGT                                                                                    |    |    | 1551 |
| CCATAAAAAA AAATGCACTG TAAGAATTAT GTCAAGGCCT AGGAGCAGGC TCAGAGTACA                                                                                    |    |    | 1611 |
| AGAGCTGTCC TTGCCAAAGG TCACTAAGGC AGGAACCGCA GAGCCAGCCA CCAGAGTCTT                                                                                    |    |    | 1671 |

GGTACTGGGT TGAGCCCCTC ACTATTCCCA GCACAGGGCC TGGCCCTGAG GTAAGCCTGT 1731  
 GCTGCTTCAG AAGTTGGCTT TTCTCCTTCT GGGATTGGTG TCCACTCTGC CCCTTTTCTA 1791  
 GGTCAATGGAG CTAGTGCAGT GTAATGTTCC CAGGAGGTAG GTACACTCTT AGGTGTTGTG 1851  
 GGGATCCAAG TGCTGGTTCC CACCATTGGC ATTAACAGTG GACTGCAAGC AGAGAGAGGG 1911  
 GTCCCCATCA TTGTTTCGTG GACACTGAGG CCTTGAGACC TTGGCTGCTG TGTCTATGTG 1971  
 GACTGGCAAA GACTGTGGCT TGGGAGGGGC TTCCTCAGCA CTGGCACCTG AACTCAGCAC 2031  
 CAAGGATGGC CCCAAGAGGC TTGTTTTCAT TTGCCTTTGT TCTCCAGTGC TTTGGTTACC 2091  
 TCAGGGCAGG GCTGAACAAT AGTGTGATGT TACATTGAAG AATAAAGACC CAACCAACAA 2151  
 ATGTTAGTGT CATTTTCAGT CTAAGTAAAT AAGCCATTAT GTCATTTCCC TTAATTCTTA 2211  
 GTAAAGTTAT GTAATTACAT AATGTAAAAA 2241

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Arg Ala Phe His Gln Thr Cys Pro Asn Phe Val Ile Glu Lys Ile Glu  
 1 5 10 15  
 Arg Ile Gln Asn Pro Ala Leu Trp Arg Arg Tyr Gln Ala Tyr Lys Lys  
 20 25 30  
 Ile Met Asp Glu Lys Asn Gly Asn Val Ile Asn Glu Lys Gln Leu Phe  
 35 40 45  
 His Gly Thr Glu Phe Gly Ser Leu Ala Gln Leu Asn Ser Asn Gly Phe  
 50 55 60  
 Asn Arg Ser Tyr Ala Gly Lys Asn Ala Thr Ala Tyr Gly Lys Gly Thr  
 65 70 75 80  
 Tyr Phe Ala Val Asn Ala Ser Tyr Ser Ala His Asp Thr Tyr Ser Lys  
 85 90 95  
 Pro Asp Ala Asn Gly Lys Lys Tyr Met Tyr Tyr Val Arg Val Leu Thr  
 100 105 110  
 Gly Asn Tyr Thr Gln Gly Asn Ala Ser Leu Ile Val Pro Pro Ser Arg  
 115 120 125  
 Asp Pro Gln Asn Ala Thr Asp Leu Phe Asp Thr Val Ala Asp Asn Val  
 130 135 140  
 Ile Asn Pro Ser Ile Phe Val Val Phe Tyr Asp Asn Gln Ala Tyr Pro  
 145 150 155 160

Glu Tyr Leu Ile Thr Phe Arg Lys  
165

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1918 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: HW049
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: complement (1289..1612)
  - (D) OTHER INFORMATION: /label= SAC\_24337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GTCGACGTGG TGATTATCTT AAAGGTAAGG GAGGTTTTTT TTTCCCTGAT ACTGATGAAG  | 60   |
| GCTGAGTGTG ACTGTTTAGT ATAGCTAGTG GGCTTTGTCA CTTAAGCCTT CCTTAGCATG  | 120  |
| TTCCCTTTCC CTTATTTTTT CTGGATACTT ACGTGCTAAC GTGCTAACAA CTCCAGATCA  | 180  |
| AACTGAGTAT GGAGATTTTT GCTTTAACAA TTTAGGAGTG GCAAACAATT TATAACTGGC  | 240  |
| AGGGTTTGAG GACAGCCGTG TTGAAAAACC AAAAGAAAAT GCTAAGGCAG GTCTTGACCA  | 300  |
| ATGTGGATAC TTTGACTAAT TAACTTCGTT ACTTTAGGAG GAGGTTGTTC CTGCACGCCA  | 360  |
| TCCATCTCCA GCGTTCGAAG GTTAGATTGT TGGGGTGGTG TGTCTTGTTT ACCAGATTGG  | 420  |
| CTGTTTCTGT GATGAATCAA CTAGCTCACT ATGACTGCTA ATGAAAACAC TGGAACACCT  | 480  |
| GAGAAACTGA AGGGTGGCGT GTTGGGGCAA GGGTGCTTAC ATATCAAGCC TTTTCAATAG  | 540  |
| TTTGTTTTTC TCCAGGTTCT GTTAGCAGTG CTGTTACTTG GTGCTTCAGA GGTAAGTAAT  | 600  |
| TGCAGCCAGC GTGCAGTGGT GTGCACACTG CTGGACTCAG GTCCTAAGTA CTTCATATAT  | 660  |
| ATGATGACTT TCATAGAATC TCGTTCGGCT GATGATTGCT GTTGAGACTT GGAAATCTGA  | 720  |
| TTTTTCTGAG GATGATGGGT TGGATGGGAA CAATCTGCCA GGATTTTTTAA CATTGCCCAT | 780  |
| CTCGTGTGTT TCAGATATGG TGA CTGGCCG AGCGCAAAGG AGCCATGCCA GGTAAATGTT | 840  |
| CTAGCAATAT TATTGTTTAT TAGGTAGATA CGTAATGGCT TGATCCAGTG CTTTCCTGCT  | 900  |
| CACCCTGATG AACTGAATAC CGCCCCAGTC TGATAGCTGT GGAGAAAGGT ATTTTCTGAG  | 960  |
| TTGAGCTCAT CTTGGATCAA ACAGGAAGGG TTTTATGCTA GTTAGTATAT GATCTCTGTA  | 1020 |

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GGATACGTTT AGGCAATAAG GATAATGACC CAAATTTATT TACTGTTTTG CAGGAAACT 1080
AAGAGCACAT CTTCATAAAG TCCAGGCTAA AGTAAGGTGA GAAACTAAG ATGTAAAGTG 1140
TACCAAGTTA GTAACCTCCC TATGAAGAAA CATTACACAG TCTTACTTCC TGTCCCTAGCT 1200
CCAGAGCCTG AAAAGGTGAA CCCACTGGGG CTGGCTGGGG GAAAAGAGGA AATTTTGTTC 1260
CAGAAGGAAC TGTCTGAGGG ATCATTGTGA TGTGTGGAAA GGAAGAATT AAACCTTGAT 1320
TAAAAAGGAA ACAAGGTGGT TTGTCTGTTT TTCAGGCTCG AGGAGAGGGA TGAGGTGTGT 1380
GTTAGAGGTA GGTAGCCCTT CAAGTCATTG TAATTAGGTG GGCAGGGTAG ATTTTGCTTT 1440
CTGCTAATTA AAACCTTTAC CTTACAGGAA CTGAAATCAA AGATCCGATT ACCTAGGCCA 1500
GTGGCACGGC AAACCTCAGA ACTCATGGAA TACAGCCTGT TGATTCCCTG TGGATTTTFA 1560
GCATCTGAGC AGTATCAGTG GCACTCCAAG TGAAATGGTT GATCTCTTCA GTACCGCTGG 1620
AGCAGATTAA TATTTATTTT ACTGCCAGAG GCTATATTTT TCTGCCCCC CATACCCCTT 1680
TCCTCTTCTC CTTAGACTAC TTAAGATTGA AATATTTGCA ACTCCAAATT TATCTTCCTT 1740
GCTTACCACT TTTTTTCCG AGCTGGGGAC CAAACCCAGG GCCTTGCCTC TCCTAGGTAA 1800
GCGCTCTATC ACTGAGCTAA ATCCCAGCC CCGCTTACCA CATTGTAAAT CTGATCCTTC 1860
CGCAGTTATT TGTGCTGTTT TTTTGTTC TGGCAATAAA TGCTTTTAT GCTAAAAA 1918

```

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3942 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: HW050

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..1326

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: complement (3542..3733)
- (D) OTHER INFORMATION: /label= SAC\_24644

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```

GTCGAC ATA AAT ATG GCC GTC CGG GTA CCC CTC GGC TGC ACG GGC TCC 48
 Ile Asn Met Ala Val Arg Val Pro Leu Gly Cys Thr Gly Ser
 1 5 10
TTC TGC CCG CGG CTG CTA CCA CTG CTG GCA TTG TTG GAG CTG CTC GTC 96

```

|                   |            |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |     |
|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-----|
| Phe<br>15         | Cys        | Pro               | Arg               | Leu               | Leu<br>20         | Pro               | Leu               | Leu               | Ala               | Leu<br>25         | Leu               | Glu               | Leu               | Leu               | Val<br>30         |     |
| GAC<br>Asp        | CCC<br>Pro | AGC<br>Ser        | TTG<br>Leu        | GGC<br>Gly<br>35  | CGC<br>Arg        | GTC<br>Val        | CAT<br>His        | CAC<br>His        | CTG<br>Leu<br>40  | GCG<br>Ala        | CTC<br>Leu        | AAA<br>Lys        | GAT<br>Asp        | GAC<br>Asp<br>45  | GTG<br>Val        | 144 |
| CGG<br>Arg        | CAC<br>His | AAA<br>Lys        | GTC<br>Val<br>50  | CAT<br>His<br>50  | CTC<br>Leu        | AAC<br>Asn        | ACC<br>Thr        | TTC<br>Phe<br>55  | GGC<br>Gly<br>55  | TTC<br>Phe        | TTC<br>Phe        | AAG<br>Lys        | GAC<br>Asp<br>60  | GGG<br>Gly        | TAC<br>Tyr        | 192 |
| ATG<br>Met        | GTG<br>Val | GTC<br>Val<br>65  | AAC<br>Asn        | ATC<br>Ile        | AGC<br>Ser        | AGC<br>Ser        | CTC<br>Leu<br>70  | TCT<br>Ser        | GTG<br>Val        | AAC<br>Asn        | GAG<br>Glu        | CCT<br>Pro<br>75  | GAG<br>Glu        | GGA<br>Gly        | GTC<br>Val        | 240 |
| AAG<br>Lys<br>80  | GAC<br>Asp | AAA<br>Lys        | GAC<br>Asp        | ACT<br>Thr        | GAG<br>Glu        | ATT<br>Ile<br>85  | GGC<br>Gly<br>85  | TTC<br>Phe        | AGT<br>Ser        | CTT<br>Leu        | GAT<br>Asp<br>90  | CGG<br>Arg        | ACC<br>Thr        | AAG<br>Lys        | AAT<br>Asn        | 288 |
| GAT<br>Asp<br>95  | GGC<br>Gly | TTT<br>Phe        | TCT<br>Ser        | TCT<br>Ser        | TAC<br>Tyr<br>100 | CTG<br>Leu        | GAT<br>Asp        | GAA<br>Glu        | GAT<br>Asp        | GTG<br>Val<br>105 | AAT<br>Asn        | TAC<br>Tyr        | TGT<br>Cys        | ATT<br>Ile        | TTA<br>Leu<br>110 | 336 |
| AAA<br>Lys        | AAA<br>Lys | AAG<br>Lys        | TCC<br>Ser        | ATG<br>Met<br>115 | TCT<br>Ser        | TCT<br>Ser        | GTC<br>Val        | ACT<br>Thr        | CTG<br>Leu<br>120 | CTC<br>Leu        | ATC<br>Ile        | TTA<br>Leu        | GAC<br>Asp        | ATC<br>Ile<br>125 | TCC<br>Ser        | 384 |
| GGA<br>Gly        | AGT<br>Ser | GGA<br>Gly        | GTC<br>Val<br>130 | AAG<br>Lys        | GTC<br>Val        | AGA<br>Arg        | TCC<br>Ser        | CCA<br>Pro<br>135 | CCA<br>Pro        | GAA<br>Glu        | GCT<br>Ala        | GGC<br>Gly        | AAG<br>Lys<br>140 | CAG<br>Gln        | TTA<br>Leu        | 432 |
| CCC<br>Pro        | GAG<br>Glu | ATT<br>Ile<br>145 | GTC<br>Val        | TTC<br>Phe        | AGC<br>Ser        | AAG<br>Lys        | GAT<br>Asp<br>150 | GAG<br>Glu        | AAA<br>Lys        | GTC<br>Val        | CCG<br>Pro        | AGT<br>Ser<br>155 | CGG<br>Arg        | AGC<br>Ser        | CAG<br>Gln        | 480 |
| GAG<br>Glu<br>160 | CCT<br>Pro | GCT<br>Ala        | GTC<br>Val        | AGC<br>Ser        | TCC<br>Ser        | AAC<br>Asn<br>165 | CCC<br>Pro        | AAA<br>Lys        | GAC<br>Asp        | AGC<br>Ser        | AAG<br>Lys<br>170 | GTG<br>Val        | CAG<br>Gln        | AGA<br>Arg        | ACC<br>Thr        | 528 |
| CCT<br>Pro<br>175 | GAT<br>Asp | GGT<br>Gly        | TCC<br>Ser        | AAG<br>Lys        | GCT<br>Ala<br>180 | CAA<br>Gln        | CGA<br>Arg        | AGT<br>Ser        | ACA<br>Thr        | GTG<br>Val<br>185 | GAT<br>Asp        | TCA<br>Ser        | AAG<br>Lys        | ACT<br>Thr        | ATA<br>Ile<br>190 | 576 |
| GCA<br>Ala        | GAG<br>Glu | AAA<br>Lys        | TTC<br>Phe<br>195 | TTC<br>Phe        | TCA<br>Ser        | ATT<br>Ile        | CAT<br>His        | AAG<br>Lys        | AAT<br>Asn<br>200 | GAT<br>Asp        | GGG<br>Gly        | GCA<br>Ala        | GTT<br>Val        | TCA<br>Ser<br>205 | TTT<br>Phe        | 624 |
| CAG<br>Gln        | TTC<br>Phe | TTC<br>Phe        | TTT<br>Phe<br>210 | AAC<br>Asn        | ATC<br>Ile        | AGC<br>Ser        | ACC<br>Thr        | AGT<br>Ser<br>215 | GAC<br>Asp        | CAG<br>Gln        | GAA<br>Glu        | GGC<br>Gly        | CTC<br>Leu<br>220 | TAC<br>Tyr        | AGC<br>Ser        | 672 |
| CTT<br>Leu        | TAC<br>Tyr | TTC<br>Phe<br>225 | CAC<br>His        | AAG<br>Lys        | TGC<br>Cys        | CCA<br>Pro        | AGC<br>Ser<br>230 | AGC<br>Ser        | AAG<br>Lys        | CTG<br>Leu        | AGG<br>Arg        | TCT<br>Ser<br>235 | GGT<br>Gly        | GAG<br>Glu        | CAG<br>Gln        | 720 |
| GTC<br>Val<br>240 | TCA<br>Ser | TTC<br>Phe        | AGC<br>Ser        | CTA<br>Leu        | AAT<br>Asn        | ATT<br>Ile<br>245 | GAT<br>Asp        | ATC<br>Ile        | ACC<br>Thr        | GAG<br>Glu        | AAG<br>Lys<br>250 | AAT<br>Asn        | CCT<br>Pro        | GAC<br>Asp        | AGC<br>Ser        | 768 |
| TAC<br>Tyr<br>255 | CTG<br>Leu | TCT<br>Ser        | GCA<br>Ala        | GGG<br>Gly        | GAA<br>Glu<br>260 | ATC<br>Ile        | CCT<br>Pro        | CTC<br>Leu        | CCC<br>Pro        | AAG<br>Lys<br>265 | TTA<br>Leu        | TAC<br>Tyr        | GTT<br>Val        | TCC<br>Ser        | ATG<br>Met<br>270 | 816 |



|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GCC TTG TTG TTC TTC CTG TCT GGG ACC GTG TGG ATT CAC ATC CTT CGT<br>Ala Leu Leu Phe Phe Leu Ser Gly Thr Val Trp Ile His Ile Leu Arg<br>275 280 285     | 864  |
| AAA CGA AGG AAT GAT GTA TTT AAA ATT CAC TGG TTG ATG GCG GCC CTT<br>Lys Arg Arg Asn Asp Val Phe Lys Ile His Trp Leu Met Ala Ala Leu<br>290 295 300     | 912  |
| CCT TTC ACC AAG TCT CTC TCC TTG GTG TTC CAT GCA ATC GAC TAC CAC<br>Pro Phe Thr Lys Ser Leu Ser Leu Val Phe His Ala Ile Asp Tyr His<br>305 310 315     | 960  |
| TAC ATC TCC TCG CAG GGC TTT CCG ATT GAA GGC TGG GCT GTT GTG TAC<br>Tyr Ile Ser Ser Gln Gly Phe Pro Ile Glu Gly Trp Ala Val Val Tyr<br>320 325 330     | 1008 |
| TAC ATA ACT CAC CTG CTG AAG GGT GCA CTG CTG TTC ATC ACC ATC GCC<br>Tyr Ile Thr His Leu Leu Lys Gly Ala Leu Leu Phe Ile Thr Ile Ala<br>335 340 345 350 | 1056 |
| CTC ATT GGC ACT GGC TGG GCC TTC ATC AAG CAC ATC CTG TCT GAT AAG<br>Leu Ile Gly Thr Gly Trp Ala Phe Ile Lys His Ile Leu Ser Asp Lys<br>355 360 365     | 1104 |
| GAC AAG AAG ATC TTC ATG ATT GTC ATT CCG CTC CAG GTA CTG GCG AAT<br>Asp Lys Lys Ile Phe Met Ile Val Ile Pro Leu Gln Val Leu Ala Asn<br>370 375 380     | 1152 |
| GTG GCC TAC ATC ATC ATA GAG TCT ACT GAG GAG GGC ACA ACT GAG TAT<br>Val Ala Tyr Ile Ile Ile Glu Ser Thr Glu Glu Gly Thr Thr Glu Tyr<br>385 390 395     | 1200 |
| GGC TTG TGG AAG GAC TCT CTA TTC CTG GTG GAT TTG CTG TGC TGC GGC<br>Gly Leu Trp Lys Asp Ser Leu Phe Leu Val Asp Leu Leu Cys Cys Gly<br>400 405 410     | 1248 |
| GCC ATC CTC TTC CCA GTG GTG TGG TCA ATC AGG CAT TTA CAA GAA GCC<br>Ala Ile Leu Phe Pro Val Val Trp Ser Ile Arg His Leu Gln Glu Ala<br>415 420 425 430 | 1296 |
| TCG GCC ACA GAT GGA AAG CTG CCA TTA ACC TAGCAAAGCT GAAGCTTTTC<br>Ser Ala Thr Asp Gly Lys Leu Pro Leu Thr<br>435 440                                   | 1346 |
| AGACATTACT ACGTCCTGAT CGTGTGCTAC ATCTACTTCA CCAGGATCAT CGCCTTTCTT                                                                                     | 1406 |
| CTCAAGTTTCG CTGTTCCCTT CCAGTGGAAG TGGCTCTACC AGCTGCTGGA TGAAACAGCC                                                                                    | 1466 |
| ACACTGGTGT TCTTTGTCCT GACGGGGTAT AAATTTTCGCC CAGCTTCAGA TAACCCCTAC                                                                                    | 1526 |
| CTGCAGCTCT CTCAGGAAGA AGATGACCTG GAGATGGAGT CTGTAGTGAC GACGTCAGGA                                                                                     | 1586 |
| GTAATGGAGA ACATGAAGAA GGTGAAGAAA GTGAGCAATG GTGCTGTGGA GCCCCAGGGC                                                                                     | 1646 |
| AGCTGGGAAG GCACCGCGTG ACAGCGCAGC TGAGGACCGC AGGCCGTCAA TGAACCTAGC                                                                                     | 1706 |
| TTATCCATAG CCCTATCAGT GAGCACGCCT GTTCCTGACA GACGATGGCA TCTCCCAGCA                                                                                     | 1766 |
| GCGACACCCC GCGCTCAGC ACCATGGCCG AGCCGAGTGC TATGGACACA CACTTTTGTA                                                                                      | 1826 |
| CTCTTAGGGA TCTGGATTGA GGTGGGCTAC AGGCAGTGAG GACTGCCCTC AGTGAGGGCG                                                                                     | 1886 |
| GAGGCTTAGA GGAGGAGTAA AGACTGTCTG TCTGATTAC CTTGCTAATT GGGAGCCTGG                                                                                      | 1946 |

|             |            |             |             |            |             |      |
|-------------|------------|-------------|-------------|------------|-------------|------|
| GTCTGTGCAG  | GGGAGCCCCC | AGTGGCTGCT  | ACTCAGAAAG  | GCTGTGGGTG | TGGCACGGGT  | 2006 |
| CTGCCACTCG  | CTGGTCACAG | TTCTGTGGAG  | GCTGGGAGGA  | TGTGACTCAC | TGCTTGCCCT  | 2066 |
| AGCATTTACG  | AGGCTTTGGG | TTCAATTCCCT | AGTGCCAGGG  | TGGGGGGAAA | AGAAGTTACT  | 2126 |
| TTGGGACTAG  | TCAGGTATCT | ACCAAGGGCA  | CAGAGAAGAG  | AAAGAGATTG | TCAGCCTTTG  | 2186 |
| GGAACAAGAA  | CAACAGAAAT | GATTGAAATT  | CTTTTAAATA  | GCCAATAAAC | CCCTAGGTGG  | 2246 |
| CAGAAGACAC  | CTGTCCAGGG | TCACTGGCCC  | CCAGGCACCA  | CTCTAAATGT | CCCTGCCCCCT | 2306 |
| GATGTGACCT  | ACAACAGTGG | TGCTAGAGGC  | CAGAGGGAGG  | GAGGGAGGGG | GCCTGTTACA  | 2366 |
| TGGCTGGCTG  | CAGGGGAGAA | GAGCCTTGCC  | TCTCCAGAAG  | TGTTCTCCAG | TTGGCTCTCA  | 2426 |
| GGACTCCATC  | CCCTGGCTGC | CTGCCCAGAG  | CAGCCGCCCTG | GCTTCCTCTC | CTTCCACCTG  | 2486 |
| TGTCTTCTGA  | TCCGAGAAAA | CAGTTTTCCT  | GAAGGAGCAG  | CCGAGGACAG | AAAGGGTAGT  | 2546 |
| CTCTAAACAA  | ACACTTAGGT | TAAGCATCTT  | CCACAGCTCG  | CATGGGCCAG | GCAGGACCTC  | 2606 |
| TGAGCCTCAG  | CTATAGTCCA | AGCATGCGTG  | AAGGAAGTGT  | TTGAGCCACT | CATGCTCAGA  | 2666 |
| GACCTGAGGC  | AGCCGGGTCT | GCTCAGAGCT  | TGGACAGGGA  | CACCAGCGGC | ACCTGCGGAA  | 2726 |
| GGCCTGTGAG  | GGGCCACAGG | AGACCAGCTC  | AGCACCTCAG  | AGCTGCTGCC | TGCCCAGAAC  | 2786 |
| TGGCGGGCGA  | GTTGCACCTT | CAAGGAACAG  | GCACTTCCGG  | GAGGGGGGTG | AGTTACTCCA  | 2846 |
| CCTCCCACTG  | CAGAAGACAA | AGGTCTGGTC  | TCCACACCAC  | ACCCCAAGTC | CCTGTCTGTG  | 2906 |
| GCCACCAGTG  | AGAAGCTGCT | GTCTGCTGCC  | CTAGCAGGTC  | CGTCACTACC | GCAGGTGCTC  | 2966 |
| CATCTTGAGA  | AAGGTCGACA | GGCCTGAAGG  | ATCCACCTAA  | AGGACCTTTT | TCTCCTGTTT  | 3026 |
| TGTTTGCTTT  | GTTTATACTT | GTTTAAAGTA  | TGTGGTGGGA  | AGGGAGTGTC | GAGGAGACAA  | 3086 |
| GGTGTTAATG  | CTTTGTCTTC | TGCACATAAG  | CACTCCTCCA  | GCACTGCAGA | AGTGTGTCCC  | 3146 |
| TGTGGTGACT  | CTAAGCCACA | GCTGTCCCTC  | AGAGGGCGCG  | ATCTTTATGG | AAGGAGCCTC  | 3206 |
| CTTTCACCTG  | CTGGGTTTTA | ATAAGGCCAC  | TCTGACAGAG  | AGCAGAGGGA | GCTGTGTACA  | 3266 |
| ACCCAGCCAC  | AGAGCTCTCT | GGGTGCACAG  | CTGAGCGGCT  | ATGGGAGACA | GCCCGCTCCT  | 3326 |
| TCCAGAGCAT  | GGGTGCACAG | GCAGGGAGGT  | GTGCTACAGC  | AGCGGCCCTC | CCAAGTCCTG  | 3386 |
| CCCTGTGACT  | GCTGTAGGTG | GGAAGCCAGG  | CATGTTGGGG  | GTTGTGGTGG | GGAGGGGGGA  | 3446 |
| TCAGAAGCCT  | AACATGGGGC | TGGGAAGAAC  | TGGCCTGGTG  | CCCAGGCTGT | GGAAAGGAAA  | 3506 |
| ACTCCCAGCC  | CTCAGCATGC | ACTGTAAGGT  | GTCTGTCTCA  | TCTGCATCGC | TTGAGAGCTG  | 3566 |
| GGAGCCCGCA  | TTCAGCAGTG | TCCTTGGGTA  | GAGGAGTCTG  | ATTGGCATCC | AGCCGCCCCA  | 3626 |
| GTTTCATGAGC | TGCCCTCTGC | AGCCTTGAGT  | CTTAGCCTAC  | CCAGCTCCAC | AACCGTGTTT  | 3686 |
| GAGTGGTGAA  | GCCCTTGTGT | TGGAGGGGCT  | GAGCAGAAAT  | GGGGTGTA   | TTGCACTGCC  | 3746 |
| ACTGTGGTAT  | TAATAGCTCT | GTGTTGTGTC  | CCCACCCCCA  | CCCCCATCT  | TCTGCCTGCG  | 3806 |

TGAGGTATCC ATACTTGT TT TGAGAGTGCT GTGGACTGGA AGCTGTGGGC TGTGACATTT 3866  
 AATAAAGTGT GGATTTTGT AGATAATTAT TTCTTGACA ACAGGAACAA GTGTTTCAGCT 3926  
 CTGAAAAAAA GTCGAC 3942

## (2) INFORMATION FOR SEQ ID NO:43:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ile Asn Met Ala Val Arg Val Pro Leu Gly Cys Thr Gly Ser Phe Cys  
 1 5 10 15  
 Pro Arg Leu Leu Pro Leu Leu Ala Leu Leu Glu Leu Leu Val Asp Pro  
 20 25 30  
 Ser Leu Gly Arg Val His His Leu Ala Leu Lys Asp Asp Val Arg His  
 35 40 45  
 Lys Val His Leu Asn Thr Phe Gly Phe Phe Lys Asp Gly Tyr Met Val  
 50 55 60  
 Val Asn Ile Ser Ser Leu Ser Val Asn Glu Pro Glu Gly Val Lys Asp  
 65 70 75 80  
 Lys Asp Thr Glu Ile Gly Phe Ser Leu Asp Arg Thr Lys Asn Asp Gly  
 85 90 95  
 Phe Ser Ser Tyr Leu Asp Glu Asp Val Asn Tyr Cys Ile Leu Lys Lys  
 100 105 110  
 Lys Ser Met Ser Ser Val Thr Leu Leu Ile Leu Asp Ile Ser Gly Ser  
 115 120 125  
 Gly Val Lys Val Arg Ser Pro Pro Glu Ala Gly Lys Gln Leu Pro Glu  
 130 135 140  
 Ile Val Phe Ser Lys Asp Glu Lys Val Pro Ser Arg Ser Gln Glu Pro  
 145 150 155 160  
 Ala Val Ser Ser Asn Pro Lys Asp Ser Lys Val Gln Arg Thr Pro Asp  
 165 170 175  
 Gly Ser Lys Ala Gln Arg Ser Thr Val Asp Ser Lys Thr Ile Ala Glu  
 180 185 190  
 Lys Phe Phe Ser Ile His Lys Asn Asp Gly Ala Val Ser Phe Gln Phe  
 195 200 205  
 Phe Phe Asn Ile Ser Thr Ser Asp Gln Glu Gly Leu Tyr Ser Leu Tyr  
 210 215 220  
 Phe His Lys Cys Pro Ser Ser Lys Leu Arg Ser Gly Glu Gln Val Ser  
 225 230 235 240

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Ser | Leu | Asn | Ile | Asp | Ile | Thr | Glu | Lys | Asn | Pro | Asp | Ser | Tyr | Leu |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Ala | Gly | Glu | Ile | Pro | Leu | Pro | Lys | Leu | Tyr | Val | Ser | Met | Ala | Leu |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Leu | Phe | Phe | Leu | Ser | Gly | Thr | Val | Trp | Ile | His | Ile | Leu | Arg | Lys | Arg |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Arg | Asn | Asp | Val | Phe | Lys | Ile | His | Trp | Leu | Met | Ala | Ala | Leu | Pro | Phe |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Thr | Lys | Ser | Leu | Ser | Leu | Val | Phe | His | Ala | Ile | Asp | Tyr | His | Tyr | Ile |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ser | Ser | Gln | Gly | Phe | Pro | Ile | Glu | Gly | Trp | Ala | Val | Val | Tyr | Tyr | Ile |
|     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     | 335 |     |
| Thr | His | Leu | Leu | Lys | Gly | Ala | Leu | Leu | Phe | Ile | Thr | Ile | Ala | Leu | Ile |
|     |     |     | 340 |     |     |     |     | 345 |     |     |     |     | 350 |     |     |
| Gly | Thr | Gly | Trp | Ala | Phe | Ile | Lys | His | Ile | Leu | Ser | Asp | Lys | Asp | Lys |
|     |     | 355 |     |     |     |     | 360 |     |     |     |     | 365 |     |     |     |
| Lys | Ile | Phe | Met | Ile | Val | Ile | Pro | Leu | Gln | Val | Leu | Ala | Asn | Val | Ala |
|     | 370 |     |     |     |     | 375 |     |     |     |     | 380 |     |     |     |     |
| Tyr | Ile | Ile | Ile | Glu | Ser | Thr | Glu | Glu | Gly | Thr | Thr | Glu | Tyr | Gly | Leu |
| 385 |     |     |     |     | 390 |     |     |     |     | 395 |     |     |     |     | 400 |
| Trp | Lys | Asp | Ser | Leu | Phe | Leu | Val | Asp | Leu | Leu | Cys | Cys | Gly | Ala | Ile |
|     |     |     |     | 405 |     |     |     |     | 410 |     |     |     |     | 415 |     |
| Leu | Phe | Pro | Val | Val | Trp | Ser | Ile | Arg | His | Leu | Gln | Glu | Ala | Ser | Ala |
|     |     |     | 420 |     |     |     |     | 425 |     |     |     |     | 430 |     |     |
| Thr | Asp | Gly | Lys | Leu | Pro | Leu | Thr |     |     |     |     |     |     |     |     |
|     |     | 435 |     |     |     |     | 440 |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1838 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW051

**(ix) FEATURE:**

- (A) NAME/KEY: CDS  
(B) LOCATION: 114..1505

**(ix) FEATURE:**

- (A) NAME/KEY: misc\_feature  
(B) LOCATION: 1411..1603  
(D) OTHER INFORMATION: /label= SAC 24170

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

|                                                                   |                 |
|-------------------------------------------------------------------|-----------------|
| GTCGACGGCT GGTTTGAAAA GTGACAACGG CCGGTGGATT TTAGGAGTTT GCTCGGTTTG | 60              |
| TAACTGCTCT TTGGTGAGCT ACTGGGACTG CAGACTAGGA GGAGACTCCC AAA ATG    | 116             |
|                                                                   | Met<br>1        |
| GAA ACT CTG TCC TTC CCC AGA TAC AAC ATA GCT GAG ATT GTA GTT CAT   | 164             |
| Glu Thr Leu Ser Phe Pro Arg Tyr Asn Ile Ala Glu Ile Val Val His   |                 |
|                                                                   | 5 10 15         |
| ATT CGC AAT AAA CTG TTA ACT GGA GCG GAT GGC AAA AAC CTC TCC AAG   | 212             |
| Ile Arg Asn Lys Leu Leu Thr Gly Ala Asp Gly Lys Asn Leu Ser Lys   |                 |
|                                                                   | 20 25 30        |
| AGC GAT TTT CTT CCA AAC CCG AAG CCT GAA GTC CTG TAC ATG ATT TAC   | 260             |
| Ser Asp Phe Leu Pro Asn Pro Lys Pro Glu Val Leu Tyr Met Ile Tyr   |                 |
|                                                                   | 35 40 45        |
| ATG AGA GCC TTA CAG TTA GTG TAT GGG GTC CGG CTG GAG CAT TTC TAC   | 308             |
| Met Arg Ala Leu Gln Leu Val Tyr Gly Val Arg Leu Glu His Phe Tyr   |                 |
|                                                                   | 50 55 60 65     |
| ATG ATG CCG GTG AAC ATA GAA GTC ATG TAT CCA CAT ATA ATG GAG GGC   | 356             |
| Met Met Pro Val Asn Ile Glu Val Met Tyr Pro His Ile Met Glu Gly   |                 |
|                                                                   | 70 75 80        |
| TTC TTA CCG GTC AGC AAT TTG TTC TTC CAC CTG GAC TCG TTT ATG CCC   | 404             |
| Phe Leu Pro Val Ser Asn Leu Phe Phe His Leu Asp Ser Phe Met Pro   |                 |
|                                                                   | 85 90 95        |
| ATT TGC CGG GTG AAT GAC TTT GAG ATC GCC GAT ATT CTT TAT CCA AAA   | 452             |
| Ile Cys Arg Val Asn Asp Phe Glu Ile Ala Asp Ile Leu Tyr Pro Lys   |                 |
|                                                                   | 100 105 110     |
| GCA AAC CCG ACA AGT CGT TTT TTA AGT GGC ATT ATC AAC TTT ATT CAC   | 500             |
| Ala Asn Arg Thr Ser Arg Phe Leu Ser Gly Ile Ile Asn Phe Ile His   |                 |
|                                                                   | 115 120 125     |
| TTC AGA GAA ACA TGC CTG GAG AAG TAT GAA GAA TTT CTT TTG CAA AAT   | 548             |
| Phe Arg Glu Thr Cys Leu Glu Lys Tyr Glu Glu Phe Leu Leu Gln Asn   |                 |
|                                                                   | 130 135 140 145 |
| AAA TCC TCT GTG GAC AAA ATA CAG CAG TTA AGC AAT GCA CAC CAG GAA   | 596             |
| Lys Ser Ser Val Asp Lys Ile Gln Gln Leu Ser Asn Ala His Gln Glu   |                 |
|                                                                   | 150 155 160     |
| GCA TTG ATG AAA CTG GAA AAA CTC AAT TCG GTT CCC GTG GAG GAG CAG   | 644             |
| Ala Leu Met Lys Leu Glu Lys Leu Asn Ser Val Pro Val Glu Glu Gln   |                 |
|                                                                   | 165 170 175     |
| GAA GAG TTC AAA CAG CTG AAG GAT GAC ATC CAG GAG CTG CAG CAC TTG   | 692             |
| Glu Glu Phe Lys Gln Leu Lys Asp Asp Ile Gln Glu Leu Gln His Leu   |                 |
|                                                                   | 180 185 190     |
| CTG AAT CAA GAC TTC AGA CAG AAA ACG ACA CTG CTG CAG GAG AGA TAT   | 740             |
| Leu Asn Gln Asp Phe Arg Gln Lys Thr Thr Leu Leu Gln Glu Arg Tyr   |                 |
|                                                                   | 195 200 205     |
| ACC AAA ATG AAA TCA GAT TTT TCA GAG AAA ACC AAG CAT GTT AAT GAG   | 788             |

|            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |            |      |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------|
| Thr<br>210 | Lys        | Met        | Lys        | Ser        | Asp<br>215 | Phe        | Ser        | Glu        | Lys        | Thr<br>220 | Lys        | His        | Val        | Asn        | Glu<br>225 |      |
| CTA<br>Leu | AAG<br>Lys | TTG<br>Leu | TCA<br>Ser | GTA<br>Val | GTT<br>Val | TCT<br>Ser | TTG<br>Leu | AAA<br>Lys | GAA<br>Glu | GTT<br>Val | CAA<br>Gln | GAC<br>Asp | AGT<br>Ser | TTG<br>Leu | AAA<br>Lys | 836  |
| AGC<br>Ser | AAA<br>Lys | ATT<br>Ile | GTG<br>Val | GAT<br>Asp | TCT<br>Ser | CCA<br>Pro | GAG<br>Glu | AAG<br>Lys | CTG<br>Leu | AAG<br>Lys | AAC<br>Asn | TAT<br>Tyr | AAA<br>Lys | GAG<br>Glu | AAG<br>Lys | 884  |
| ATG<br>Met | AAG<br>Lys | GAC<br>Asp | ACC<br>Thr | GTC<br>Val | CAG<br>Gln | AAG<br>Lys | CTC<br>Leu | CGC<br>Arg | AGT<br>Ser | GCC<br>Ala | AGG<br>Arg | GAA<br>Glu | GAA<br>Glu | GTG<br>Val | ATG<br>Met | 932  |
| GAG<br>Glu | AAG<br>Lys | TAT<br>Tyr | GAT<br>Asp | ATC<br>Ile | TAT<br>Tyr | AGA<br>Arg | GAT<br>Asp | TCT<br>Ser | GTG<br>Val | GAT<br>Asp | TGC<br>Cys | TTG<br>Leu | CCT<br>Pro | TCC<br>Ser | TGT<br>Cys | 980  |
| CAG<br>Gln | CTG<br>Leu | GAG<br>Glu | GTG<br>Val | CAG<br>Gln | TTA<br>Leu | TAT<br>Tyr | CAA<br>Gln | AAG<br>Lys | AAA<br>Lys | TCA<br>Ser | CAG<br>Gln | GAC<br>Asp | CTT<br>Leu | GCA<br>Ala | GAT<br>Asp | 1028 |
| AAT<br>Asn | AGG<br>Arg | GAG<br>Glu | AAA<br>Lys | CTA<br>Leu | AGC<br>Ser | AGT<br>Ser | ATC<br>Ile | TTA<br>Leu | AAG<br>Lys | GAG<br>Glu | AGC<br>Ser | CTG<br>Leu | AAC<br>Asn | CTG<br>Leu | GAG<br>Glu | 1076 |
| GGC<br>Gly | CAG<br>Gln | ATT<br>Ile | GAT<br>Asp | AGT<br>Ser | GAT<br>Asp | TCA<br>Ser | TCA<br>Ser | GAA<br>Glu | CTA<br>Leu | AAG<br>Lys | AAA<br>Lys | CTG<br>Leu | AAG<br>Lys | ACT<br>Thr | GAA<br>Glu | 1124 |
| GAG<br>Glu | AAC<br>Asn | TCC<br>Ser | CTC<br>Leu | ATA<br>Ile | AGA<br>Arg | CTG<br>Leu | ATG<br>Met | ACT<br>Thr | CTA<br>Leu | AAG<br>Lys | AAG<br>Lys | GAG<br>Glu | AGA<br>Arg | CTT<br>Leu | GCT<br>Ala | 1172 |
| ACC<br>Thr | ATG<br>Met | CAG<br>Gln | TTC<br>Phe | AAA<br>Lys | ATA<br>Ile | AAC<br>Asn | AAG<br>Lys | AAG<br>Lys | CAG<br>Gln | GAG<br>Glu | GAT<br>Asp | GTG<br>Val | AAA<br>Lys | CAG<br>Gln | TAC<br>Tyr | 1220 |
| AAG<br>Lys | CGG<br>Arg | ACC<br>Thr | ATG<br>Met | ATT<br>Ile | GAA<br>Glu | GAT<br>Asp | TGC<br>Cys | AAT<br>Asn | AAA<br>Lys | GTT<br>Val | CAA<br>Gln | GAA<br>Glu | AAA<br>Lys | AGA<br>Arg | GAT<br>Asp | 1268 |
| GCT<br>Ala | GTC<br>Val | TGC<br>Cys | GAG<br>Glu | CAA<br>Gln | GTA<br>Val | ACC<br>Thr | GCC<br>Ala | ATT<br>Ile | AAT<br>Asn | CAA<br>Gln | GAC<br>Asp | ATC<br>Ile | CAC<br>His | AAG<br>Lys | ATT<br>Ile | 1316 |
| AAA<br>Lys | TCT<br>Ser | GGG<br>Gly | ATT<br>Ile | CAG<br>Gln | CAG<br>Gln | CTA<br>Leu | AGA<br>Arg | GAC<br>Asp | GCC<br>Ala | GAA<br>Glu | AAA<br>Lys | CGG<br>Arg | GAG<br>Glu | AAA<br>Lys | CTG<br>Leu | 1364 |
| AAG<br>Lys | TCT<br>Ser | CAG<br>Gln | GAA<br>Glu | ATC<br>Ile | TTG<br>Leu | GTA<br>Val | GAC<br>Asp | TTG<br>Leu | AAA<br>Lys | AGT<br>Ser | GCT<br>Ala | TTG<br>Leu | GAG<br>Glu | AAG<br>Lys | TAC<br>Tyr | 1412 |
| CAT<br>His | GAG<br>Glu | GGC<br>Gly | ATC<br>Ile | GAG<br>Glu | AAG<br>Lys | ACG<br>Thr | ACG<br>Thr | GAG<br>Glu | GAG<br>Glu | TGC<br>Cys | TGC<br>Cys | ACT<br>Thr | AGA<br>Arg | ATA<br>Ile | GGA<br>Gly | 1460 |
| GGG<br>Gly | AAG<br>Lys | ACT<br>Thr | GCC<br>Ala | GAG<br>Glu | CTG<br>Leu | AAG<br>Lys | AGG<br>Arg | AGG<br>Arg | ATG<br>Met | TTC<br>Phe | AAA<br>Lys | ATG<br>Met | CCG<br>Pro | CCC<br>Pro |            | 1505 |

TGATCAACAG CCACCCGAAA ATGGCCTTTC GCTTCTGTGTT TGGAGTAGTT ATATTGAAGC 1565  
 TAATAGAAGG ACCGCAGTCT CAGCTAACTA GCGTGGGTAC CATTGTTCT CTGTCCTTTT 1625  
 ATGACCATGT GCTCCCTGTG TTTTCTCTT GGTGATGGGG ATACAACTCA GGGCCTTGCA 1685  
 GGCTACACTG ACTTGCTCC CTAGGCTCTA ATGTACCATG TACTATGTAG GCTTTTGCTA 1745  
 CAATTAAAGT AACGTGTACA GCTTTTATGT CCCTACTCTG TCTCCTTTTG TATGTGCTGG 1805  
 TTGGAATAAA CAAATAGTTA CTGACGTCAA AAA 1838

## (2) INFORMATION FOR SEQ ID NO:45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 464 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Glu Thr Leu Ser Phe Pro Arg Tyr Asn Ile Ala Glu Ile Val Val  
 1 5 10 15  
 His Ile Arg Asn Lys Leu Leu Thr Gly Ala Asp Gly Lys Asn Leu Ser  
 20 25 30  
 Lys Ser Asp Phe Leu Pro Asn Pro Lys Pro Glu Val Leu Tyr Met Ile  
 35 40 45  
 Tyr Met Arg Ala Leu Gln Leu Val Tyr Gly Val Arg Leu Glu His Phe  
 50 55 60  
 Tyr Met Met Pro Val Asn Ile Glu Val Met Tyr Pro His Ile Met Glu  
 65 70 75 80  
 Gly Phe Leu Pro Val Ser Asn Leu Phe Phe His Leu Asp Ser Phe Met  
 85 90 95  
 Pro Ile Cys Arg Val Asn Asp Phe Glu Ile Ala Asp Ile Leu Tyr Pro  
 100 105 110  
 Lys Ala Asn Arg Thr Ser Arg Phe Leu Ser Gly Ile Ile Asn Phe Ile  
 115 120 125  
 His Phe Arg Glu Thr Cys Leu Glu Lys Tyr Glu Glu Phe Leu Leu Gln  
 130 135 140  
 Asn Lys Ser Ser Val Asp Lys Ile Gln Gln Leu Ser Asn Ala His Gln  
 145 150 155 160  
 Glu Ala Leu Met Lys Leu Glu Lys Leu Asn Ser Val Pro Val Glu Glu  
 165 170 175  
 Gln Glu Glu Phe Lys Gln Leu Lys Asp Asp Ile Gln Glu Leu Gln His  
 180 185 190  
 Leu Leu Asn Gln Asp Phe Arg Gln Lys Thr Thr Leu Leu Gln Glu Arg  
 195 200 205

Tyr Thr Lys Met Lys Ser Asp Phe Ser Glu Lys Thr Lys His Val Asn  
 210 215 220  
 Glu Leu Lys Leu Ser Val Val Ser Leu Lys Glu Val Gln Asp Ser Leu  
 225 230 235 240  
 Lys Ser Lys Ile Val Asp Ser Pro Glu Lys Leu Lys Asn Tyr Lys Glu  
 245 250 255  
 Lys Met Lys Asp Thr Val Gln Lys Leu Arg Ser Ala Arg Glu Glu Val  
 260 265 270  
 Met Glu Lys Tyr Asp Ile Tyr Arg Asp Ser Val Asp Cys Leu Pro Ser  
 275 280 285  
 Cys Gln Leu Glu Val Gln Leu Tyr Gln Lys Lys Ser Gln Asp Leu Ala  
 290 295 300  
 Asp Asn Arg Glu Lys Leu Ser Ser Ile Leu Lys Glu Ser Leu Asn Leu  
 305 310 315 320  
 Glu Gly Gln Ile Asp Ser Asp Ser Ser Glu Leu Lys Lys Leu Lys Thr  
 325 330 335  
 Glu Glu Asn Ser Leu Ile Arg Leu Met Thr Leu Lys Lys Glu Arg Leu  
 340 345 350  
 Ala Thr Met Gln Phe Lys Ile Asn Lys Lys Gln Glu Asp Val Lys Gln  
 355 360 365  
 Tyr Lys Arg Thr Met Ile Glu Asp Cys Asn Lys Val Gln Glu Lys Arg  
 370 375 380  
 Asp Ala Val Cys Glu Gln Val Thr Ala Ile Asn Gln Asp Ile His Lys  
 385 390 395 400  
 Ile Lys Ser Gly Ile Gln Gln Leu Arg Asp Ala Glu Lys Arg Glu Lys  
 405 410 415  
 Leu Lys Ser Gln Glu Ile Leu Val Asp Leu Lys Ser Ala Leu Glu Lys  
 420 425 430  
 Tyr His Glu Gly Ile Glu Lys Thr Thr Glu Glu Cys Cys Thr Arg Ile  
 435 440 445  
 Gly Gly Lys Thr Ala Glu Leu Lys Arg Arg Met Phe Lys Met Pro Pro  
 450 455 460

## (2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1483 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:



(B) CLONE: HW052

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 247..765

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: complement (660..1062)

(D) OTHER INFORMATION: /label= SAC\_24882

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GTCGACCAAA AACAGGACAG ATTGCAACAG CCTCTACACT TCCTTCATGG CCTGCTCTTG | 60  |
| GGCCGTGGCG ACAAGCAGAA AGAAGCTTGA TTGTGGAGAG GTGCCCTAGC GGAGGGATGT | 120 |
| CTGCCACAGT CCAGGCACCC CACAGAGGGT AGGAGCTCCA TGTACGAGTG GCTTTGCATT | 180 |
| TCTTCAGAAA AGAATAGCTG ATGTGCAATC TCAGCCTTTC TGCAGAAGGA TTTATCAGGG | 240 |
| GCCAGC ATG GGC TCT GTG AAT TCT AGA GGC CAT AAG GCC CAG GTG GTA    | 288 |
| Met Gly Ser Val Asn Ser Arg Gly His Lys Ala Gln Val Val           |     |
| 1 5 10                                                            |     |
| ATG CTG GGC CTC GAC TGT GCT GGC AAG ACC ACA ATC CTG TAC AAA CTG   | 336 |
| Met Leu Gly Leu Asp Cys Ala Gly Lys Thr Thr Ile Leu Tyr Lys Leu   |     |
| 15 20 25 30                                                       |     |
| AAA GGA AAC CGG CTG GTG GAT ACC CTA CCC ACT GTT GGT TTT AAT GTA   | 384 |
| Lys Gly Asn Arg Leu Val Asp Thr Leu Pro Thr Val Gly Phe Asn Val   |     |
| 35 40 45                                                          |     |
| GAG CCT CTT GAG GCT CCT GGA CAT GTG TCG CTG ACT CTC TGG GAC ATT   | 432 |
| Glu Pro Leu Glu Ala Pro Gly His Val Ser Leu Thr Leu Trp Asp Ile   |     |
| 50 55 60                                                          |     |
| GGG GGA CAG ACC CAG CTC AGG GCT ACG TGG AAG GAC TAC CTG GAA GGC   | 480 |
| Gly Gly Gln Thr Gln Leu Arg Ala Thr Trp Lys Asp Tyr Leu Glu Gly   |     |
| 65 70 75                                                          |     |
| ATT GAC CTC CTT GTG TAC GTG CTG GAC AGC ACA GAT GAA GCC CGC TTG   | 528 |
| Ile Asp Leu Leu Val Tyr Val Leu Asp Ser Thr Asp Glu Ala Arg Leu   |     |
| 80 85 90                                                          |     |
| CCC GAG GCA GTG GCT GAG CTC GAG GAA GTC CTA GAA GAC CCC AAC ATG   | 576 |
| Pro Glu Ala Val Ala Glu Leu Glu Glu Val Leu Glu Asp Pro Asn Met   |     |
| 95 100 105 110                                                    |     |
| GCT GGT GTT CCT TTC TTG GTA CTG GCC AAC AAG CAG GAG GCT CCT GAT   | 624 |
| Ala Gly Val Pro Phe Leu Val Leu Ala Asn Lys Gln Glu Ala Pro Asp   |     |
| 115 120 125                                                       |     |
| GCT CTA CCA TTG CTT GAA ATC AGA AAC AGG CTG GAC CTG GAA AGG TTC   | 672 |
| Ala Leu Pro Leu Leu Glu Ile Arg Asn Arg Leu Asp Leu Glu Arg Phe   |     |
| 130 135 140                                                       |     |
| CAA GAC CAT TGC TGG GAG CTG CGG GCT TGC AGC GCT CTC ACA GGT CAG   | 720 |
| Gln Asp His Cys Trp Glu Leu Arg Ala Cys Ser Ala Leu Thr Gly Gln   |     |
| 145 150 155                                                       |     |
| GGG CTA CAG GAA GCC CGG CAG AGC CTG CTG CAT TTG CTG AGA TCC       | 765 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gly | Leu | Gln | Glu | Ala | Arg | Gln | Ser | Leu | Leu | His | Leu | Leu | Arg | Ser |  |
| 160 |     |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |  |

  

|            |            |             |            |            |             |      |
|------------|------------|-------------|------------|------------|-------------|------|
| TGATGAAATG | CAGTAACCTC | TAACCTCCAGG | CTGGAGCAGG | ACAGGGAGCA | GGGTCAGCCA  | 825  |
| GACCCCTGA  | GCAGGCAAAT | AGATTATCCT  | TGCTTCTAAG | AACAGGAGGG | GCCAGCTGAT  | 885  |
| CCTTGAGAAA | GTGAAGCTCC | GTTTGCCACA  | TGAGAAACCA | CGTTTCTCTT | GGACGGTGTG  | 945  |
| TTTTCTTCTC | AGGACTTCTT | CTCAGTGGCG  | GTTATGCGGA | AAATCAACTG | TTCTTCAAGT  | 1005 |
| AACAATCGTC | AGAGGGAATA | TAAAAACCCCT | CAGAATACCC | CCATGTAACA | GCTCAGTACC  | 1065 |
| AAGTGTCAAA | GTCACAAACT | TGGTGACATA  | ATTATTGATG | ACCAAGTTCA | CAAATGAAAA  | 1125 |
| GAGGTTTCAA | AACTACATCT | GAGTGTCACT  | GGGCCTATCG | CTGTTATCCG | AGTGTCACCTG | 1185 |
| GGCCTATCAT | TGTCATCCGA | GTGTCACCAG  | GCCTATCACG | GTCATCTGCC | TGTCACTGGG  | 1245 |
| CCTATCACAG | TCATCAGGAG | CGACTCTTCC  | TACTGGCCTT | GGGGCAGAAG | CCACTGTCAC  | 1305 |
| TGGTGGGCTC | ACAGCAGGAG | GGGCAGGTCT  | GCTCTCATAA | TGTCGCAGAA | GGCAGAAGTC  | 1365 |
| CATGGGGCCC | TAGATCCTCC | CAGAAATCCC  | CCTGATCTCC | AACTCTGACT | AACTCTTTTC  | 1425 |
| TGCCCTATAT | CCTCTGTTGT | AAAAAAGTAA  | AATAAACTC  | CTCTTATACT | CTCAAAAA    | 1483 |

## (2) INFORMATION FOR SEQ ID NO:47:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gly | Ser | Val | Asn | Ser | Arg | Gly | His | Lys | Ala | Gln | Val | Val | Met | Leu |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |

  

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Leu | Asp | Cys | Ala | Gly | Lys | Thr | Thr | Ile | Leu | Tyr | Lys | Leu | Lys | Gly |
|     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |     |

  

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Arg | Leu | Val | Asp | Thr | Leu | Pro | Thr | Val | Gly | Phe | Asn | Val | Glu | Pro |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |

  

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Glu | Ala | Pro | Gly | His | Val | Ser | Leu | Thr | Leu | Trp | Asp | Ile | Gly | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

  

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Thr | Gln | Leu | Arg | Ala | Thr | Trp | Lys | Asp | Tyr | Leu | Glu | Gly | Ile | Asp |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |

  

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Leu | Val | Tyr | Val | Leu | Asp | Ser | Thr | Asp | Glu | Ala | Arg | Leu | Pro | Glu |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |

  

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Val | Ala | Glu | Leu | Glu | Glu | Val | Leu | Glu | Asp | Pro | Asn | Met | Ala | Gly |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |

  

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Phe | Leu | Val | Leu | Ala | Asn | Lys | Gln | Glu | Ala | Pro | Asp | Ala | Leu |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |

Pro Leu Leu Glu Ile Arg Asn Arg Leu Asp Leu Glu Arg Phe Gln Asp  
 130 135 140

His Cys Trp Glu Leu Arg Ala Cys Ser Ala Leu Thr Gly Gln Gly Leu  
 145 150 155 160

Gln Glu Ala Arg Gln Ser Leu Leu His Leu Leu Arg Ser  
 165 170

## (2) INFORMATION FOR SEQ ID NO:48:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

(B) CLONE: HW054

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1952..2152
- (D) OTHER INFORMATION: /label= SAC\_24183

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GTCTACGGTG GGGTCTAACT GAGGTCTTGT ATTTGGTTTT TCCTGAAGAT CGACCTCTGG | 60  |
| CATCAGGAGG CTTGAGCAAG GAGAAGAGTG GATGATGAAG GAAAGAGACA AGGAAAGAAA | 120 |
| GAGAAGTGTG CACAAAGAAA CTTGTATTAT TATTAATTAG CACCTAGCTT GTTTGTGTCT | 180 |
| GATACACCAC CAAGTAGTAA TTGTTGAAAA AAGCGAAGAA GAAAAAAAAA AAAACAAAAA | 240 |
| AACCAAACAG TGGGTACTCA AATAAGATAG GAGAAAAATG AAGAGAACAG ACCCAGTTCT | 300 |
| CGACCCTTGC TTCTCGAAGG TCCTCCCACC AGGCTGCCAA AGCAAGATGG TGTGCTCTG  | 360 |
| ATCCAGTCAG TATTCTTTTG ACTTTTTTTT TTAATCTCCA GGTTTTGGTT CAGGCTCCCA | 420 |
| TATTCATACC CTGGCTCATT TAGCTTTCCC TCATGTTGTG GGTCTTCTG TCCCTCACCC  | 480 |
| CCTTACTCTC CCCACTGATA TTCTTCCCAC GTCAAGACTG TGGCTCTGGA AGAAATATCC | 540 |
| ACCATTTGCA GAGCTGATGT TCTGTAGATC GTAATGTTGA AGCGCTGGGT GTCCTGGTTG | 600 |
| GCAGAATCAC TCCTGTATTA CTCTGGTACA TAGGTGTCTC CTGNTAGACT CCCTGGCCTT | 660 |
| AGTCATGGGG TGTTTTCTAG AGGCAGACTA AGACAGGAGT CAAAAAGAT TTAGAGGAAG  | 720 |
| GAGCTGAGGA AAGAAAGACA GTTGTGGGAG GAAAATCAAG TTCTACTCAG GATCCCAGT  | 780 |
| GTTTCTGTAG ATGTAGATTG GAATGTGTCC ATAACAGAGA GGCCAGTGAG AGACATCCCC | 840 |

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AAGGACCTGC CAGGCTTTCC TTCGCTCCAG GAAGACGCAC CATCACTCAA AAGGGGTTTC 900
CTAGAAAGAA AGACAAGTGA CTTAAAAAAT CTGCCAGTGG GTTCTTGAAG TCATCGAACC 960
TAGGAGGTAG AAAGCTCACG GGGGTCATGT TATCGAAGGG AGGTGAGGTT CAGTCAGGCT 1020
AACTATTAGG GAGANTGTCA AAGGAGGCTA CAGAAATGGG ATTCTGGCTG TGGGGCATT A 1080
AAGGCTATCA AGTCAACAGG TAAGAGTGGG GTGGCTCAGC AGCTTCTCTG GCGCTGAAAG 1140
TGGTGTCTCT TAACAGTTAA TTCCCTTCCC TTTTCCATCA CAGAAGGAAT CATTCCAGCC 1200
CTCCCTGGGA TTATGGTCCC CCAGTGACCA TGTTCATCT GCTGGATTTT TGATCAGTTT 1260
AGAAGGAAAA AAACACTTGG GTTCGGTGGT ATTTGCTTAT GACCTTAGCA CTTTGGAGCT 1320
GAGAAGAGGA TTGCCATAGT TTCCAGACCA GTCTGGTTTA CATAGTGAGT TCTAGGGCTG 1380
CGTAATGAGA TGTCTCAAGA ATGGAGAGGG GCGTTAGGGA GAACTTACTT AGCTCTTCAA 1440
GAAACTGTCC TGTAACAAA GAGAAATGAG TCGATGGGTG ACCAGTGGGA GCCTNCCCCC 1500
CACCTCCTCA GACAACCTT CTTTTCCATT AAGGGGCCTG TGCATCTCAG TAAGTGGTCC 1560
TCAGTTTTCC TGAGGATTCT GATGGTGAGA GTAGAGAGAG CAAAAGATT CTCAGCCCTG 1620
GGATCTAGAA CCTTGGTTCC ACTCTTTTCC CGTTCTGGTC TGCCTGAGCT CCCCCCCCCC 1680
GCCCCCAGT GGTCTGTGTT GCTGTCCAGA CATTGCACCT GCCAGTCTTC GGTGCAGCCA 1740
GTTGTAGCAG ATGATCAAAG CAACCAGNGG TCCAAGAACA GGGACAATCA ACAAACAGTG 1800
TTATCTTCCA GCAGGGCACT CTCAGGAAGT GAGGATCTGA ATGGTAAAGC AGAACAGAGT 1860
GTTTCCCTCT ATGCCACAGC CGCTCATGCC ACACCCACTT GAAGCCTCCA AAGCCAGNAC 1920
AAGCTGTAGA GTCCATGAAT GTAGATGAGG TACATTGTGC GCCTTGCTTT TACTTCCTTT 1980
AGCTTCTGAT TGAATTTAGC TGTATCTTTT TAACCGATTT ATCGTAGAAN ACAATGGGTG 2040
GTGTGACCCT NTCATGCTTT GTTGATCTTC AGCCACACGC TGCCCTCCCT CGCCCCCACT 2100
TCTAGCATTT GTGTGTGTGC GCGTGTTTTT TTGAAGAGGG GTTNTTGCTT GTACAATCCC 2160
TGGCTGGCCT TGAACCTGAG AAGTCCTCCT GCCTCCGCCT TCCAGGTGCT GGGATTACAA 2220
GTTGTCAACC CTGCTTTCAC TAATGTTTCC TTTTATTAA AGATTATTT ATTATTAAA 2280
AAGTCGAC

```

## (2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2349 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: HW055

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 214..1329

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1953..2065  
(D) OTHER INFORMATION: /label= SAC\_24449

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GTGACAATG CTTTCAAGCA AACAGCCGCT ACCAGAACAA CTCTGTGACT AGGAGAAAGA   | 60  |
| GGCCAAGGCG CGAGTTCCCA AACCCCTGAAG CCACAGGAGC CCAAGGGGGA GACTGGAGAG | 120 |
| AAGGTATTTT TAGCCGTGCA CAGTGACTGA TCAGCCGAGG ACCTACCCTC GAGTTCTATT  | 180 |
| CTGCAACAGT GAACAGTGAA GGTCTCCAAA GAG ATG GAG TAC GAG GGT TAC AAC   | 234 |
| Met Glu Tyr Glu Gly Tyr Asn                                        |     |
| 1 5                                                                |     |
| GAC TCC AGC ATC TAC GGT GAG GAG TAT TCT GAC GGC TCG GAC TAC ATC    | 282 |
| Asp Ser Ser Ile Tyr Gly Glu Glu Tyr Ser Asp Gly Ser Asp Tyr Ile    |     |
| 10 15 20                                                           |     |
| GTG GAC TTG GAG GAG GCG GGT CCA CTG GAG GCC AAG GTG GCC GAG GTC    | 330 |
| Val Asp Leu Glu Glu Ala Gly Pro Leu Glu Ala Lys Val Ala Glu Val    |     |
| 25 30 35                                                           |     |
| TTC CTG GTG GTA ATC TAC AGC TTG GTG TGC TTC CTC GGG ATC CTA GGC    | 378 |
| Phe Leu Val Val Ile Tyr Ser Leu Val Cys Phe Leu Gly Ile Leu Gly    |     |
| 40 45 50 55                                                        |     |
| AAT GGC CTG GTG ATT GTC ATC GCC ACC TTC AAG ATG AAG AAG ACG GTG    | 426 |
| Asn Gly Leu Val Ile Val Ile Ala Thr Phe Lys Met Lys Lys Thr Val    |     |
| 60 65 70                                                           |     |
| AAC ACC GTG TGG TTT GTC AAC CTG GCC GTG GCT GAC TTC CTG TTC AAC    | 474 |
| Asn Thr Val Trp Phe Val Asn Leu Ala Val Ala Asp Phe Leu Phe Asn    |     |
| 75 80 85                                                           |     |
| ATC TTC TTG CCC ATC CAC ATC ACC TAT GCC GCT ATG GAC TAC CAC TGG    | 522 |
| Ile Phe Leu Pro Ile His Ile Thr Tyr Ala Ala Met Asp Tyr His Trp    |     |
| 90 95 100                                                          |     |
| GTG TTC GGG AAA GCC ATG TGC AAG ATT AGT AGC TTT CTG CTA AGC CAC    | 570 |
| Val Phe Gly Lys Ala Met Cys Lys Ile Ser Ser Phe Leu Leu Ser His    |     |
| 105 110 115                                                        |     |
| AAC ATG TAC ACC AGC GTC TTC CTG CTC ACT GTC ATC AGC TTC GAC CGC    | 618 |
| Asn Met Tyr Thr Ser Val Phe Leu Leu Thr Val Ile Ser Phe Asp Arg    |     |
| 120 125 130 135                                                    |     |
| TGC ATC TCC GTG CTC CTC CCC GTC TGG TCC CAG AAC CAC CGC AGC GTG    | 666 |
| Cys Ile Ser Val Leu Leu Pro Val Trp Ser Gln Asn His Arg Ser Val    |     |
| 140 145 150                                                        |     |
| CGT CTG GCC TAC ATG ACC TGC GTG GTT GTC TGG GTC CTG GCT TTC TTC    | 714 |
| Arg Leu Ala Tyr Met Thr Cys Val Val Val Trp Val Leu Ala Phe Phe    |     |

| 155               |                   |                   |                   |                   |                   |                   | 160               |                   |                   |                   |                   | 165               |                   |                   |                   |      |      |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|------|------|
| CTG<br>Leu        | AGT<br>Ser        | TCC<br>Ser<br>170 | CCG<br>Pro        | TCC<br>Ser        | CTC<br>Leu        | GTC<br>Val        | TTC<br>Phe<br>175 | CGG<br>Arg        | GAC<br>Asp        | ACG<br>Thr        | GTC<br>Val        | AGC<br>Ser<br>180 | ACC<br>Thr        | AGC<br>Ser        | CAC<br>His        | 762  |      |      |
| GGG<br>Gly        | AAG<br>Lys<br>185 | ATA<br>Ile        | ACC<br>Thr        | TGC<br>Cys        | TTC<br>Phe        | AAC<br>Asn<br>190 | AAC<br>Asn        | TTC<br>Phe        | AGC<br>Ser        | CTG<br>Leu        | GCC<br>Ala<br>195 | GCG<br>Ala        | CCC<br>Pro        | GAG<br>Glu        | CCT<br>Pro        | 810  |      |      |
| TTC<br>Phe<br>200 | TCT<br>Ser        | CAT<br>His        | TCC<br>Ser        | ACC<br>Thr        | CAC<br>His<br>205 | CCG<br>Pro        | CGA<br>Arg        | ACA<br>Thr        | GAC<br>Asp        | CCG<br>Pro<br>210 | GTA<br>Val        | GGG<br>Gly        | TAC<br>Tyr        | AGC<br>Ser        | AGA<br>Arg<br>215 | 858  |      |      |
| CAT<br>His        | GTG<br>Val        | GCG<br>Ala        | GTC<br>Val        | ACC<br>Thr<br>220 | GTC<br>Val        | ACC<br>Thr        | CGC<br>Arg        | TTC<br>Phe        | CTC<br>Leu<br>225 | TGT<br>Cys        | GGC<br>Gly        | TTC<br>Phe        | CTG<br>Leu        | ATC<br>Ile<br>230 | CCC<br>Pro        | 906  |      |      |
| GTC<br>Val        | TTC<br>Phe        | ATC<br>Ile        | ATC<br>Ile<br>235 | ACG<br>Thr        | GCC<br>Ala        | TGT<br>Cys        | TAC<br>Tyr        | CTC<br>Leu<br>240 | ACC<br>Thr        | ATC<br>Ile        | GTC<br>Val        | TTC<br>Phe        | AAG<br>Lys<br>245 | TTG<br>Leu        | CAG<br>Gln        | 954  |      |      |
| CGC<br>Arg        | AAC<br>Asn<br>250 | CGC<br>Arg        | CTG<br>Leu        | GCC<br>Ala        | AAG<br>Lys        | ACC<br>Thr        | AAG<br>Lys<br>255 | AAG<br>Lys        | CCC<br>Pro        | TTC<br>Phe        | AAG<br>Lys        | ATC<br>Ile<br>260 | ATC<br>Ile        | ATC<br>Ile        | ACC<br>Thr        | 1002 |      |      |
| ATC<br>Ile        | ATC<br>Ile<br>265 | ATC<br>Ile        | ACC<br>Thr        | TTC<br>Phe        | TTC<br>Phe        | CTC<br>Leu<br>270 | TGC<br>Cys        | TGG<br>Trp        | TGC<br>Cys        | CCC<br>Pro        | TAC<br>Tyr<br>275 | CAC<br>His        | ACA<br>Thr        | CTC<br>Leu        | TAC<br>Tyr        | 1050 |      |      |
| CTG<br>Leu<br>280 | CTG<br>Leu        | GAG<br>Glu        | CTC<br>Leu        | CAC<br>His        | CAC<br>His<br>285 | ACG<br>Thr        | GCT<br>Ala        | GTG<br>Val        | CCA<br>Pro        | GCC<br>Ala<br>290 | TCT<br>Ser        | GTC<br>Val        | TTC<br>Phe        | AGC<br>Ser        | CTG<br>Leu<br>295 | 1098 |      |      |
| GGA<br>Gly        | CTG<br>Leu        | CCC<br>Pro        | CTG<br>Leu        | GCC<br>Ala<br>300 | ACA<br>Thr        | GCC<br>Ala        | GTT<br>Val        | GCC<br>Ala        | ATC<br>Ile<br>305 | GCC<br>Ala        | AAC<br>Asn        | AGC<br>Ser        | TGT<br>Cys        | ATG<br>Met<br>310 | AAC<br>Asn        | 1146 |      |      |
| CCC<br>Pro        | ATC<br>Ile        | CTG<br>Leu        | TAC<br>Tyr<br>315 | GTC<br>Val        | TTC<br>Phe        | ATG<br>Met        | GGC<br>Gly        | CAC<br>His<br>320 | GAC<br>Asp        | TTC<br>Phe        | AAA<br>Lys        | AAA<br>Lys        | TTC<br>Phe<br>325 | AAG<br>Lys        | GTG<br>Val        | 1194 |      |      |
| GCC<br>Ala        | CTT<br>Leu        | TTC<br>Phe<br>330 | TCC<br>Ser        | CGC<br>Arg        | CTG<br>Leu        | GTG<br>Val        | AAT<br>Asn<br>335 | GCC<br>Ala        | CTG<br>Leu        | AGC<br>Ser        | GAG<br>Glu        | GAC<br>Asp<br>340 | ACA<br>Thr        | GGA<br>Gly        | CCC<br>Pro        | 1242 |      |      |
| TCC<br>Ser        | TCC<br>Ser        | TAC<br>Tyr<br>345 | CCC<br>Pro        | AGT<br>Ser        | CAC<br>His        | AGG<br>Arg<br>350 | AGC<br>Ser        | TTC<br>Phe        | ACC<br>Thr        | AAG<br>Lys<br>355 | ATG<br>Met        | TCC<br>Ser        | TCA<br>Ser        | TTG<br>Leu        | ATT<br>Ile        | 1290 |      |      |
| GAG<br>Glu<br>360 | AAG<br>Lys        | GCT<br>Ala        | TCA<br>Ser        | GTG<br>Val        | AAT<br>Asn<br>365 | GAG<br>Glu        | AAA<br>Lys        | GAG<br>Glu        | ACC<br>Thr        | AGC<br>Ser<br>370 | ACC<br>Thr        | CTC<br>Leu        | TGAGCCTTCC        |                   |                   | 1339 |      |      |
| CTGGGACTGT        |                   |                   | CCCCAATGGG        |                   |                   | CTCCACAGCC        |                   |                   | CAGGGACTTG        |                   |                   | TCTCCTGAGG        |                   |                   | TAGGAGACAC        |      | 1399 |      |
| GCCTGGAGCC        |                   |                   | TTTGGGTATG        |                   |                   | CCCCAGCGCC        |                   |                   | CGCTACGTCT        |                   |                   | TGCGCAAGGC        |                   |                   | GGCCCATTTGT       |      |      | 1459 |
| TTTGGGTGGA        |                   |                   | GTTCCCAAGT        |                   |                   | GTGGACACTC        |                   |                   | TTCCAGCAAA        |                   |                   | ATGGCAGACA        |                   |                   | AGCAACCTGA        |      |      | 1519 |
| GCCCTGTCAG        |                   |                   | CAGGAGTATA        |                   |                   | GGACCAACTT        |                   |                   | CCACCGGCTC        |                   |                   | AGAAAAGGGA        |                   |                   | GGGTCTCTGA        |      |      | 1579 |
| AACCAAGGTC        |                   |                   | TGAGCTGTGA        |                   |                   | CCCACATACA        |                   |                   | GGCACACAAT        |                   |                   | TTCACTGTGG        |                   |                   | ATGCCCAAA         |      |      | 1639 |

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CATGCTGCAC AGTCTCCAGT GTGGGTGAGG ACGTCACTGC AGACCTGTTA TGGCGACATG 1699
ACAGTCAAAC CAGCAAATAC CCCACCACCA CTGTCATCCT CCAAGATCTT GACTTTGGAT 1759
TTCAGAAAAA TGGGGAGGAC CAGGACCTGA GGGGCTTCAT AGAACTTGCT TGCAAGGGCA 1819
GCCCAGGTGT GTGTGTGTGT ATGTGCTTGT GTGTGTGTGT GTGTGTATGT GCATGTGTGT 1879
GTGTGTGTGT GTGTGTGTGT GTGTGTGTTG AAGAGGTGGA GACAGAGAGC AGAGAACCCC 1939
AAAGGATGTG GGTACAGGAT ATCTCACACC ATCATGCCAC AGGGAGACAG AGCTACAACG 1999
ATGGGTGCTT GGGGGTTCAG ATGGTGGCAG CTCTTTGCTT CAGTGTGTAT ACCCCCCTAG 2059
CACTGTACCC CCAGGCTGGA GGGGGGCTCT TCACAGAAGC TTCCAACCCA TTCCAGCACT 2119
GGCTGGAAGG GCTTGGGATG TCCCTGGAGA CTGGTCTGGG ACTATCTTCA AAGCGTCTTC 2179
CAAAGGCTGC TGCTGACCAG CTCACCTGAC TCCTCCTTGA ACACACTCCC CACGTGGGGC 2239
ATCACAGCCC CGATGGCAGC CCAGGATCAG GCCTCCCTCC CTTGACAGGG AAATGACTCA 2299
CCCAACCCCA TGCACGTGCA GTAACAAAGA CCCAGGCCCA GCTCCAAAAA 2349

```

## (2) INFORMATION FOR SEQ ID NO:50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```

Met Glu Tyr Glu Gly Tyr Asn Asp Ser Ser Ile Tyr Gly Glu Glu Tyr
 1 5 10 15
Ser Asp Gly Ser Asp Tyr Ile Val Asp Leu Glu Glu Ala Gly Pro Leu
 20 25 30
Glu Ala Lys Val Ala Glu Val Phe Leu Val Val Ile Tyr Ser Leu Val
 35 40 45
Cys Phe Leu Gly Ile Leu Gly Asn Gly Leu Val Ile Val Ile Ala Thr
 50 55 60
Phe Lys Met Lys Lys Thr Val Asn Thr Val Trp Phe Val Asn Leu Ala
 65 70 75 80
Val Ala Asp Phe Leu Phe Asn Ile Phe Leu Pro Ile His Ile Thr Tyr
 85 90 95
Ala Ala Met Asp Tyr His Trp Val Phe Gly Lys Ala Met Cys Lys Ile
 100 105 110
Ser Ser Phe Leu Leu Ser His Asn Met Tyr Thr Ser Val Phe Leu Leu
 115 120 125
Thr Val Ile Ser Phe Asp Arg Cys Ile Ser Val Leu Leu Pro Val Trp
 130 135 140

```

Ser Gln Asn His Arg Ser Val Arg Leu Ala Tyr Met Thr Cys Val Val  
 145 150 155 160  
 Val Trp Val Leu Ala Phe Phe Leu Ser Ser Pro Ser Leu Val Phe Arg  
 165 170 175  
 Asp Thr Val Ser Thr Ser His Gly Lys Ile Thr Cys Phe Asn Asn Phe  
 180 185 190  
 Ser Leu Ala Ala Pro Glu Pro Phe Ser His Ser Thr His Pro Arg Thr  
 195 200 205  
 Asp Pro Val Gly Tyr Ser Arg His Val Ala Val Thr Val Thr Arg Phe  
 210 215 220  
 Leu Cys Gly Phe Leu Ile Pro Val Phe Ile Ile Thr Ala Cys Tyr Leu  
 225 230 235 240  
 Thr Ile Val Phe Lys Leu Gln Arg Asn Arg Leu Ala Lys Thr Lys Lys  
 245 250 255  
 Pro Phe Lys Ile Ile Ile Thr Ile Ile Ile Thr Phe Phe Leu Cys Trp  
 260 265 270  
 Cys Pro Tyr His Thr Leu Tyr Leu Leu Glu Leu His His Thr Ala Val  
 275 280 285  
 Pro Ala Ser Val Phe Ser Leu Gly Leu Pro Leu Ala Thr Ala Val Ala  
 290 295 300  
 Ile Ala Asn Ser Cys Met Asn Pro Ile Leu Tyr Val Phe Met Gly His  
 305 310 315 320  
 Asp Phe Lys Lys Phe Lys Val Ala Leu Phe Ser Arg Leu Val Asn Ala  
 325 330 335  
 Leu Ser Glu Asp Thr Gly Pro Ser Ser Tyr Pro Ser His Arg Ser Phe  
 340 345 350  
 Thr Lys Met Ser Ser Leu Ile Glu Lys Ala Ser Val Asn Glu Lys Glu  
 355 360 365  
 Thr Ser Thr Leu  
 370

## (2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2577 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: HW056
- (ix) FEATURE:



(A) NAME/KEY: CDS  
(B) LOCATION: 8..523

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: complement (738..953)  
(D) OTHER INFORMATION: /label= SAC\_24326

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

|            |            |            |             |            |            |     |     |     |     |     |     |     |     |     |     |
|------------|------------|------------|-------------|------------|------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GTCGACG    | GGC        | TAC        | CTT         | AGC        | CAG        | CTG | ATG | CTT | CCA | GTG | ACA | GAG | CCA | CTT | 49  |
|            | Gly        | Tyr        | Leu         | Ser        | Gln        | Leu | Met | Leu | Pro | Val | Thr | Glu | Pro | Leu |     |
|            | 1          |            |             |            | 5          |     |     |     |     | 10  |     |     |     |     |     |
| TGT        | CCT        | TTG        | CAC         | AGC        | CTG        | ACA | CCC | TAT | CAG | GTC | CCC | TTC | AAT | GCA | GTT |
| Cys        | Pro        | Leu        | His         | Ser        | Leu        | Thr | Pro | Tyr | Gln | Val | Pro | Phe | Asn | Ala | Val |
| 15         |            |            |             |            | 20         |     |     |     |     | 25  |     |     |     |     | 30  |
| GCT        | ATC        | CGG        | GTC         | ACG        | CAC        | GCC | GAC | GTT | GCA | CCT | ACC | CAC | ATA | CTG | TAC |
| Ala        | Ile        | Arg        | Val         | Thr        | His        | Ala | Asp | Val | Ala | Pro | Thr | His | Ile | Leu | Tyr |
|            |            |            |             | 35         |            |     |     |     | 40  |     |     |     |     | 45  |     |
| GCT        | ATG        | AAT        | GCC         | AGC        | TGG        | GTC | GGC | CTT | TGC | AAG | ATT | GTG | GAT | GAT | ATG |
| Ala        | Met        | Asn        | Ala         | Ser        | Trp        | Val | Gly | Leu | Cys | Lys | Ile | Val | Asp | Asp | Met |
|            |            | 50         |             |            |            |     |     | 55  |     |     |     |     | 60  |     |     |
| AAA        | GGC        | TAC        | ACT         | CGG        | GGC        | CCC | ATT | CTG | CTG | GCC | CAG | AAC | CCC | ATA | TGT |
| Lys        | Gly        | Tyr        | Thr         | Arg        | Gly        | Pro | Ile | Leu | Leu | Ala | Gln | Asn | Pro | Ile | Cys |
|            | 65         |            |             |            |            |     | 70  |     |     |     |     | 75  |     |     |     |
| GAC        | TGT        | TTG        | GGC         | TTT        | GGT        | ATC | TGC | AGA | GGC | ATT | GAC | ATG | GAC | AAG | CGG |
| Asp        | Cys        | Leu        | Gly         | Phe        | Gly        | Ile | Cys | Arg | Gly | Ile | Asp | Met | Asp | Lys | Arg |
|            | 80         |            |             |            |            | 85  |     |     |     |     | 90  |     |     |     |     |
| CTG        | TAC        | CAC        | ATC         | CTC        | ACC        | CCT | CTA | CCA | CCA | GAG | GAG | TTA | AGA | ACT | GTG |
| Leu        | Tyr        | His        | Ile         | Leu        | Thr        | Pro | Leu | Pro | Pro | Glu | Glu | Leu | Arg | Thr | Val |
| 95         |            |            |             |            | 100        |     |     |     |     | 105 |     |     |     |     | 110 |
| AAC        | TGT        | CTG        | CTG         | GTT        | GGC        | ACC | ATT | TCC | ATT | CCA | CAT | TGT | ATT | TTC | AAG |
| Asn        | Cys        | Leu        | Leu         | Val        | Gly        | Thr | Ile | Ser | Ile | Pro | His | Cys | Ile | Phe | Lys |
|            |            |            |             | 115        |            |     |     |     | 120 |     |     |     |     | 125 |     |
| AAT        | CAG        | CCT        | GGG         | ACT        | GAA        | GGG | ACA | GTT | CCT | TAT | GTC | ACC | AGG | GAT | TAT |
| Asn        | Gln        | Pro        | Gly         | Thr        | Glu        | Gly | Thr | Val | Pro | Tyr | Val | Thr | Arg | Asp | Tyr |
|            |            | 130        |             |            |            |     |     | 135 |     |     |     |     | 140 |     |     |
| AAT        | TTA        | AAA        | CTT         | CTT        | GGA        | GCA | TCA | GAG | AAA | ATT | GGG | GAG | AGA | GAG | TAT |
| Asn        | Leu        | Lys        | Leu         | Leu        | Gly        | Ala | Ser | Glu | Lys | Ile | Gly | Glu | Arg | Glu | Tyr |
|            | 145        |            |             |            |            |     | 150 |     |     |     | 155 |     |     |     |     |
| AGA        | AAT        | ATA        | CTA         | CCT        | AGA        | CAC | AAA | TCA | CGG | CAA | AGA | AGA | AAA |     |     |
| Arg        | Asn        | Ile        | Leu         | Pro        | Arg        | His | Lys | Ser | Arg | Gln | Arg | Arg | Lys |     |     |
|            | 160        |            |             |            |            | 165 |     |     |     |     | 170 |     |     |     |     |
| TGAAGCCTGG | GTGTACAGAG | AGACTTTCGC | CTCGACACAT  | TGTCCCCAAG | CCTAGAGTCA |     |     |     |     |     |     |     |     |     | 583 |
| GCAGACTGAG | CGGGCTGTGT | GGCTGCTGAC | CTCGTGCCCA  | TGCCCAGTGT | TCATATAACT |     |     |     |     |     |     |     |     |     | 643 |
| GGAAAATGTG | CTGTGGTAAG | AGTCATTCAA | GCCCCTTTCGT | TTTTTTCCCC | TCTAAGACAT |     |     |     |     |     |     |     |     |     | 703 |
| GGAGGGCCTC | ATATAGCTCA | GACTGGCCTC | AGTACTCTGG  | TCCTCCTGTC | TCACTGTCCA |     |     |     |     |     |     |     |     |     | 763 |

|            |            |            |             |            |            |      |
|------------|------------|------------|-------------|------------|------------|------|
| AGGGCTGCGC | ATCCGGCTTT | TGGTCTCATA | CTTGGCCCAG  | ACCTTGCCGA | CTGGTTGTCC | 823  |
| TGGGTGTGTG | GTGCTCCTGG | AGAGCTGGGA | AGCATTGAAG  | AAAGCTGTGG | TGTCCTCCAA | 883  |
| GAAGACCAGG | GCCACAAAAG | TGTGCCTAGA | AACTGAGTAG  | CAGGCTGACC | ACAGGTTCTC | 943  |
| GGGTGCAGTG | TACGGACTGG | CAGGGACCTG | AGCAGGCTCA  | GTGGCCGTGA | GTAAGAGGCT | 1003 |
| TACTCCGTTG | AACCTTGTGG | ACCTTAGCAC | CCCAGTGTGG  | CGGCTCATTG | GCCTGATCCT | 1063 |
| TTGATGCTTG | CCATCGAATC | TCCCAATGCT | GCAATCAAGT  | GTTAGAGGAC | GGTACGTCGT | 1123 |
| CTTGTTAATT | TCTGGGTCTT | TAATCATGAG | GCTTTATGTT  | GAAGAACTTG | CTCTGACATT | 1183 |
| CAGAAAGCCT | CACGTTAGTT | AAAGAAATCC | ATGGTTCCTT  | AATTCTGGGG | ATGTTCTGAC | 1243 |
| AGACCTTGAG | GCTGTAGATA | CGTCAGAAAG | CCTCCATGTT  | AGTTAAGGAA | ATCCATGGTT | 1303 |
| CCCTAATTCT | GGGGATGTTT | TGACTGGGAA | TGTTCTGACA  | GACCTTGAGG | CTGAGATACT | 1363 |
| ACCATGGGCC | CACTAGCCTG | GGACAGGCAC | ACATATGCCT  | GGCTTGGGCA | GACCTTTGCT | 1423 |
| ATCAACGATT | TCTTCTAAGG | CCCCAGAGGC | CACTGCAAGT  | GGATGTTGCA | ATCCGGAGTG | 1483 |
| ACTGGGTCGG | GTCATTTTTG | TGGTTGCAAA | GCAGGACCCT  | GAGGAGCCTC | TTGGGCTGGC | 1543 |
| ATGATGGATC | TGACAAGACT | CCACCTTGCA | TGGAATCAGG  | AAGGACCAAG | GCTATGGAAG | 1603 |
| GCTCACAACA | TTGATTGTCT | CCGTCTTGTC | TGTAGTCATA  | GGAGTGTGGC | CAGTCTCCTC | 1663 |
| TGCTTGGCGC | CATCTTTGTG | GTGGCCTCAG | CATCTGAAAA  | TCCTCCGAGG | AGGCAGAGCT | 1723 |
| GCCTCTTCTG | GATTAGTCGG | ATTCCCTGTA | GATCACTCGG  | GCTCACAAC  | ACTCCCTGCC | 1783 |
| CCACCCCCAA | CACCATCTCT | GTCTCACTTG | AGCTTGTGGT  | GAGCCTTTGC | AGAGGGGAGG | 1843 |
| AGCTCTTCCT | GCCCAGGCAC | TCTCTGGGCT | CCTGATCCTC  | AAGCCTCTGC | TTCTTGGGTG | 1903 |
| CTCAGATCAC | AGGTGTGTGC | CGTCTTAGCC | TTGCGGACAG  | TTTTAAGACA | GCCTTGGTCA | 1963 |
| CCTTCATCTC | CCTCCCCGGG | TCTTCTTGTC | TTCACAATAA  | AGATCCCGAG | TCCAAAAAAA | 2023 |
| AAAAAAAAAA | AAATTCCAGG | AGGAAATCTG | GGTGCACAGA  | ACTTATCTGA | GTCGGCTTTG | 2083 |
| GTGAAGGAGA | TCCTCAAGGA | GCAGGAGAAC | AGGAAGGGCC  | TCATAGCTGC | CATCTGTGCG | 2143 |
| GGTCCTACGG | CCCTGCTGGC | TCACGAAGTA | GGCTTTGGAT  | GCAAGGTTAC | ATCGCACCCA | 2203 |
| TTGGCTAAGG | ACAAAATGAT | GAACGGCAGT | CACTACAGCT  | ACTCAGAGAG | CCGTGTGGAG | 2263 |
| AAGGACGGCC | TCATCCTCAC | CAGCCGTGGG | CCTGGGACCA  | GCTTCGAGTT | TGCGCTGGCC | 2323 |
| ATTGTGGAGG | CACTCAGTGG | CAAGGACATG | GCTAACCAAG  | TGAAGGCCCC | GCTTGTCTCT | 2383 |
| AAAGACTAGA | GCCCAAGCCC | TGGACCCTGG | ACCCCCAGGC  | TGAGCAGGCA | TTGGAAGCCC | 2443 |
| ACTAGTGTGT | CCACAGCCCA | GTGAACCTCA | GGAACCTAACG | TGTGAAGTAG | CCCGCTGCTC | 2503 |
| AGGAATCTCG | CCCTGGCTCT | GTACTATTCT | GAGCCTTGCT  | AGTAGAATAA | ACAGTTCCCC | 2563 |
| AAGCTCCTGA | AAAA       |            |             |            |            | 2577 |

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```

Gly Tyr Leu Ser Gln Leu Met Leu Pro Val Thr Glu Pro Leu Cys Pro
 1 5 10 15
Leu His Ser Leu Thr Pro Tyr Gln Val Pro Phe Asn Ala Val Ala Ile
 20 25 30
Arg Val Thr His Ala Asp Val Ala Pro Thr His Ile Leu Tyr Ala Met
 35 40 45
Asn Ala Ser Trp Val Gly Leu Cys Lys Ile Val Asp Asp Met Lys Gly
 50 55 60
Tyr Thr Arg Gly Pro Ile Leu Leu Ala Gln Asn Pro Ile Cys Asp Cys
 65 70 75 80
Leu Gly Phe Gly Ile Cys Arg Gly Ile Asp Met Asp Lys Arg Leu Tyr
 85 90 95
His Ile Leu Thr Pro Leu Pro Pro Glu Glu Leu Arg Thr Val Asn Cys
 100 105 110
Leu Leu Val Gly Thr Ile Ser Ile Pro His Cys Ile Phe Lys Asn Gln
 115 120 125
Pro Gly Thr Glu Gly Thr Val Pro Tyr Val Thr Arg Asp Tyr Asn Leu
 130 135 140
Lys Leu Leu Gly Ala Ser Glu Lys Ile Gly Glu Arg Glu Tyr Arg Asn
 145 150 155 160
Ile Leu Pro Arg His Lys Ser Arg Gln Arg Arg Lys
 165 170

```

## (2) INFORMATION FOR SEQ ID NO:53:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: HW057

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..1023

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 1032..1176

(D) OTHER INFORMATION: /label= SAC\_23926

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

|        |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GTCGAC | GGC | GCG | CTG | GAG | GAC | GCA | CGG | CTT | GGC | GGG | AAG | GCG | AGG | GGA | 48  |
|        | Gly | Ala | Leu | Glu | Asp | Ala | Arg | Leu | Gly | Gly | Lys | Ala | Arg | Gly |     |
|        | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     |
| CCG    | TGC | GGA | GCC | TCC | GGT | GCT | GGC | GGC | GGC | CAC | CAG | TTC | GGG | AGC | CGG |
| Pro    | Cys | Gly | Ala | Ser | Gly | Ala | Gly | Gly | Gly | His | Gln | Phe | Gly | Ser | Arg |
| 15     |     |     |     | 20  |     |     |     | 25  |     |     |     |     |     | 30  |     |
| GAG    | CCG | GCC | GCA | GCA | CGC | GGA | ACA | GAG | CAG | AGG | GTG | GCG | GGG | CCC | GGC |
| Glu    | Pro | Ala | Ala | Ala | Arg | Gly | Thr | Glu | Gln | Arg | Val | Ala | Gly | Pro | Gly |
|        |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |
| GAA    | ACC | ACG | ATG | AAG | CCG | AAC | AGC | GAG | GAA | GAG | GAG | GAG | TTG | GTG | CAG |
| Glu    | Thr | Thr | Met | Lys | Pro | Asn | Ser | Glu | Glu | Glu | Glu | Glu | Leu | Val | Gln |
|        |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |
| GGC    | GTG | GGC | CCC | TGG | GAC | GAG | TGC | TTC | GAG | GTG | GCC | GTG | CAG | TTG | GCG |
| Gly    | Val | Gly | Pro | Trp | Asp | Glu | Cys | Phe | Glu | Val | Ala | Val | Gln | Leu | Ala |
|        |     | 65  |     |     |     | 70  |     |     |     |     |     | 75  |     |     |     |
| TTG    | CGT | GCG | GGA | CAA | ATC | ATC | AGA | AAG | GCC | CTC | ACT | GAG | GAA | AAA | CAC |
| Leu    | Arg | Ala | Gly | Gln | Ile | Ile | Arg | Lys | Ala | Leu | Thr | Glu | Glu | Lys | His |
|        | 80  |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |
| GTC    | TCG | ACG | AAA | ACA | TCT | GCT | GCA | GAT | CTT | GTG | ACA | GAA | ACA | GAT | CAC |
| Val    | Ser | Thr | Lys | Thr | Ser | Ala | Ala | Asp | Leu | Val | Thr | Glu | Thr | Asp | His |
|        | 95  |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |
| CGA    | GTA | GAA | GAC | TTA | ATT | GTT | TCT | GAG | TTG | CGA | AAG | CGG | TTC | CCT | TCA |
| Arg    | Val | Glu | Asp | Leu | Ile | Val | Ser | Glu | Leu | Arg | Lys | Arg | Phe | Pro | Ser |
|        |     |     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |
| CAC    | AGG | TTC | ATT | GCA | GAA | GAG | GCC | ACA | GCC | TCC | GGG | GCC | AAG | TGT | GTG |
| His    | Arg | Phe | Ile | Ala | Glu | Glu | Ala | Thr | Ala | Ser | Gly | Ala | Lys | Cys | Val |
|        |     |     | 130 |     |     |     | 135 |     |     |     |     |     | 140 |     |     |
| CTC    | ACC | CAC | AGC | CCG | ACC | TGG | ATC | ATC | GAC | CCC | ATC | GAC | GGC | ACC | TGC |
| Leu    | Thr | His | Ser | Pro | Thr | Trp | Ile | Ile | Asp | Pro | Ile | Asp | Gly | Thr | Cys |
|        |     | 145 |     |     |     |     | 150 |     |     |     | 155 |     |     |     |     |
| AAC    | TTT | GTG | CAC | AGA | TTC | CCC | ACT | GTG | GCA | GTT | AGC | ATC | GGA | TTT | GCT |
| Asn    | Phe | Val | His | Arg | Phe | Pro | Thr | Val | Ala | Val | Ser | Ile | Gly | Phe | Ala |
|        | 160 |     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |
| GTT    | CAC | CAG | GAG | CTG | GAA | TTC | GGA | GTG | ATT | CAC | CAC | TGC | ACA | GAG | GAG |
| Val    | His | Gln | Glu | Leu | Glu | Phe | Gly | Val | Ile | His | His | Cys | Thr | Glu | Glu |
|        | 175 |     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |
| CGG    | CTG | TAC | ACC | GGC | AGG | AGG | GGC | CAG | GGC | GCC | TTT | TGC | AAT | GGC | CAG |
| Arg    | Leu | Tyr | Thr | Gly | Arg | Arg | Gly | Gln | Gly | Ala | Phe | Cys | Asn | Gly | Gln |
|        |     |     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |
| AGG    | CTC | CAG | GTC | TCC | AGG | GAG | ACA | GAT | CTC | GCA | AAG | GCC | TTG | GTT | CTG |
| Arg    | Leu | Gln | Val | Ser | Arg | Glu | Thr | Asp | Leu | Ala | Lys | Ala | Leu | Val | Leu |

| 210                                                                                                                                                   | 215 | 220 |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|------|
| ACA GAA ATC GGG CCC AAA CGT GAC CCC GAT ACT CTG AAA GTA TTC CTG<br>Thr Glu Ile Gly Pro Lys Arg Asp Pro Asp Thr Leu Lys Val Phe Leu<br>225 230 235     |     |     | 720  |
| AGC AAC ATG GAG CGG CTG CTG CAC GCC AAG GCT CAT GGG GTC CGA GTG<br>Ser Asn Met Glu Arg Leu Leu His Ala Lys Ala His Gly Val Arg Val<br>240 245 250     |     |     | 768  |
| ATT GGC AGC TCC ACC TTG GCG CTC TGC TAC TTG GCC TCG GGG GCT GCT<br>Ile Gly Ser Ser Thr Leu Ala Leu Cys Tyr Leu Ala Ser Gly Ala Ala<br>255 260 265 270 |     |     | 816  |
| GAT GCC TAT TAC CAG TTC GGC CTC CAC TGC TGG GAT CTG GCA GCT GCC<br>Asp Ala Tyr Tyr Gln Phe Gly Leu His Cys Trp Asp Leu Ala Ala Ala<br>275 280 285     |     |     | 864  |
| ACA GTC ATC ATC AGA GAA GCA GGT GGC ATT GTG ATT GAC ACC TCA GGT<br>Thr Val Ile Ile Arg Glu Ala Gly Gly Ile Val Ile Asp Thr Ser Gly<br>290 295 300     |     |     | 912  |
| GGA CCC CTT GAC CTC ATG TCG TGC AGA GTG GTG GCT GCT GGC ACC AGA<br>Gly Pro Leu Asp Leu Met Ser Cys Arg Val Val Ala Ala Gly Thr Arg<br>305 310 315     |     |     | 960  |
| GAG ATG GCA GTG CTC ATA GCT CAG GCC CTA CAA ACC ATT AAC TAC GGC<br>Glu Met Ala Val Leu Ile Ala Gln Ala Leu Gln Thr Ile Asn Tyr Gly<br>320 325 330     |     |     | 1008 |
| CGG GAC GAT GAG AAG TGAGCCGTAC AGAGCTCTAA GGCTGACATG AGCAGCTCCC<br>Arg Asp Asp Glu Lys<br>335                                                         |     |     | 1063 |
| TGGGAAAGAG CTGTCCGGGG GCTTGAGTTC CGGGATAGTC TACCATAGCT GTCCCCGGAC                                                                                     |     |     | 1123 |
| CTCGGTGCTT AGCTGATCCT CTCTAATCTC GGGTAGCCCC TTTCCAGGTC GGTACATGGT                                                                                     |     |     | 1183 |
| CTTTCATCAG AGCCAAACCC AAATCTTGTTG AGGTGTGTTA GTCACCCATC CTGGTTGTTC                                                                                    |     |     | 1243 |
| GGAATGCAAA TCTCAGGTAA TAAAGCTTTA GAACGAGCTC TCAGGCCCTC CCCTGCCCCGT                                                                                    |     |     | 1303 |
| GGTGATACAG AATGCAATAA ATCAGAACTT TAAAAA                                                                                                               |     |     | 1339 |

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gly Ala Leu Glu Asp Ala Arg Leu Gly Gly Lys Ala Arg Gly Pro Cys  
1 5 10 15

Gly Ala Ser Gly Ala Gly Gly Gly His Gln Phe Gly Ser Arg Glu Pro  
20 25 30

Ala Ala Ala Arg Gly Thr Glu Gln Arg Val Ala Gly Pro Gly Glu Thr

| 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Met | Lys | Pro | Asn | Ser | Glu | Glu | Glu | Glu | Glu | Leu | Val | Gln | Gly | Val |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Gly | Pro | Trp | Asp | Glu | Cys | Phe | Glu | Val | Ala | Val | Gln | Leu | Ala | Leu | Arg |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |
| Ala | Gly | Gln | Ile | Ile | Arg | Lys | Ala | Leu | Thr | Glu | Glu | Lys | His | Val | Ser |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Lys | Thr | Ser | Ala | Ala | Asp | Leu | Val | Thr | Glu | Thr | Asp | His | Arg | Val |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Glu | Asp | Leu | Ile | Val | Ser | Glu | Leu | Arg | Lys | Arg | Phe | Pro | Ser | His | Arg |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Phe | Ile | Ala | Glu | Glu | Ala | Thr | Ala | Ser | Gly | Ala | Lys | Cys | Val | Leu | Thr |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| His | Ser | Pro | Thr | Trp | Ile | Ile | Asp | Pro | Ile | Asp | Gly | Thr | Cys | Asn | Phe |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Val | His | Arg | Phe | Pro | Thr | Val | Ala | Val | Ser | Ile | Gly | Phe | Ala | Val | His |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |
| Gln | Glu | Leu | Glu | Phe | Gly | Val | Ile | His | His | Cys | Thr | Glu | Glu | Arg | Leu |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |
| Tyr | Thr | Gly | Arg | Arg | Gly | Gln | Gly | Ala | Phe | Cys | Asn | Gly | Gln | Arg | Leu |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |
| Gln | Val | Ser | Arg | Glu | Thr | Asp | Leu | Ala | Lys | Ala | Leu | Val | Leu | Thr | Glu |
|     |     | 210 |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |
| Ile | Gly | Pro | Lys | Arg | Asp | Pro | Asp | Thr | Leu | Lys | Val | Phe | Leu | Ser | Asn |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |
| Met | Glu | Arg | Leu | Leu | His | Ala | Lys | Ala | His | Gly | Val | Arg | Val | Ile | Gly |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |
| Ser | Ser | Thr | Leu | Ala | Leu | Cys | Tyr | Leu | Ala | Ser | Gly | Ala | Ala | Asp | Ala |
|     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |     |     |
| Tyr | Tyr | Gln | Phe | Gly | Leu | His | Cys | Trp | Asp | Leu | Ala | Ala | Ala | Thr | Val |
|     |     | 275 |     |     |     |     | 280 |     |     |     |     | 285 |     |     |     |
| Ile | Ile | Arg | Glu | Ala | Gly | Gly | Ile | Val | Ile | Asp | Thr | Ser | Gly | Gly | Pro |
|     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |     |     |
| Leu | Asp | Leu | Met | Ser | Cys | Arg | Val | Val | Ala | Ala | Gly | Thr | Arg | Glu | Met |
| 305 |     |     |     |     | 310 |     |     |     |     | 315 |     |     |     |     | 320 |
| Ala | Val | Leu | Ile | Ala | Gln | Ala | Leu | Gln | Thr | Ile | Asn | Tyr | Gly | Arg | Asp |
|     |     |     |     | 325 |     |     |     | 330 |     |     |     |     |     | 335 |     |
| Asp | Glu | Lys |     |     |     |     |     |     |     |     |     |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2285 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: HW059

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 9..1271

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 1991..2162  
 (D) OTHER INFORMATION: /label= SAC\_24457

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GTGACAG CCC GCC ACT CCA GGC GCG ATG CTG TTC TGG ACT GTG CTC AGC | 50  |
| Pro Ala Thr Pro Gly Ala Met Leu Phe Trp Thr Val Leu Ser         |     |
| 1 5 10                                                          |     |
| ATG GCT TTG AGT CTG CGG TTG GCA CTG GCG CAG AGC GGC ATA GAG CGC | 98  |
| Met Ala Leu Ser Leu Arg Leu Ala Leu Ala Gln Ser Gly Ile Glu Arg |     |
| 15 20 25 30                                                     |     |
| GGT CCC ACA GCA TCA GCC CCC CAG GGG GAC CTG TTG TTC CTG CTG GAC | 146 |
| Gly Pro Thr Ala Ser Ala Pro Gln Gly Asp Leu Leu Phe Leu Leu Asp |     |
| 35 40 45                                                        |     |
| AGC TCA GCC AGT GTG TCA CAC TAT GAG TTC TCA AGA GTT CGA GAG TTT | 194 |
| Ser Ser Ala Ser Val Ser His Tyr Glu Phe Ser Arg Val Arg Glu Phe |     |
| 50 55 60                                                        |     |
| GTG GGG CAG CTG GTG GCT ACG ATG CCT TTC GGA CCC GGG GCT CTG CGT | 242 |
| Val Gly Gln Leu Val Ala Thr Met Pro Phe Gly Pro Gly Ala Leu Arg |     |
| 65 70 75                                                        |     |
| GCT AGT CTG GTG CAC GTG GGC AGC CGG CCT CAC ACG GAG TTT ACT TTT | 290 |
| Ala Ser Leu Val His Val Gly Ser Arg Pro His Thr Glu Phe Thr Phe |     |
| 80 85 90                                                        |     |
| GAT CAG TAC AGT TCA GGC CAG GCC ATA CAG GAT GCT GTA CGT GTT GCG | 338 |
| Asp Gln Tyr Ser Ser Gly Gln Ala Ile Gln Asp Ala Val Arg Val Ala |     |
| 95 100 105 110                                                  |     |
| CCC CAA CGT ATG GGT GAC ACC AAC ACG GGC CTG GCA CTG GCT TAT GCC | 386 |
| Pro Gln Arg Met Gly Asp Thr Asn Thr Gly Leu Ala Leu Ala Tyr Ala |     |
| 115 120 125                                                     |     |
| AAA GAA CAA TTA TTT GCT GAG GAA GCA GGT GCC CGG CTA GGG GTT CCC | 434 |
| Lys Glu Gln Leu Phe Ala Glu Glu Ala Gly Ala Arg Leu Gly Val Pro |     |
| 130 135 140                                                     |     |
| AAG GTA CTG GTG TGG GTG ACA GAT GGG GCC TCC AGT GAC TCT GTG GGC | 482 |
| Lys Val Leu Val Trp Val Thr Asp Gly Ala Ser Ser Asp Ser Val Gly |     |
| 145 150 155                                                     |     |

|                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| CCC<br>Pro<br>160 | CCT<br>Pro<br>160 | ATG<br>Met        | CAG<br>Gln        | GAG<br>Glu        | CTC<br>Leu        | AAG<br>Lys<br>165 | GAC<br>Asp        | CTG<br>Leu        | GGT<br>Gly        | GTC<br>Val<br>170 | ACC<br>Thr<br>170 | ATC<br>Ile        | TTC<br>Phe        | ATT<br>Ile        | GTC<br>Val        | 530  |
| AGC<br>Ser<br>175 | ACT<br>Thr        | GGC<br>Gly        | CGA<br>Arg        | GGC<br>Gly        | AAC<br>Asn<br>180 | CTG<br>Leu        | TTG<br>Leu        | GAG<br>Glu        | CTG<br>Leu        | TTG<br>Leu<br>185 | GCA<br>Ala        | GCT<br>Ala        | GCC<br>Ala        | TCA<br>Ser        | GCT<br>Ala<br>190 | 578  |
| CCG<br>Pro        | GCT<br>Ala        | GAG<br>Glu        | AAG<br>Lys        | CAC<br>His<br>195 | CTA<br>Leu        | CAC<br>His        | TTT<br>Phe        | GTG<br>Val        | GAT<br>Asp<br>200 | GTG<br>Val        | GAT<br>Asp        | GAC<br>Asp        | CTT<br>Leu        | CCT<br>Pro<br>205 | ATC<br>Ile        | 626  |
| ATT<br>Ile        | GCC<br>Ala        | CGG<br>Arg        | GAG<br>Glu<br>210 | CTT<br>Leu        | CGG<br>Arg        | GGT<br>Gly        | GCC<br>Ala<br>215 | ATT<br>Ile        | ATT<br>Ile        | GAT<br>Asp        | GCG<br>Ala        | ATG<br>Met        | CAG<br>Gln<br>220 | CCA<br>Pro        | CAT<br>His        | 674  |
| CAG<br>Gln        | CTT<br>Leu        | CAT<br>His<br>225 | GCT<br>Ala        | TCG<br>Ser        | GAG<br>Glu        | ATT<br>Ile        | CTG<br>Leu<br>230 | TCC<br>Ser        | AAT<br>Asn        | GGC<br>Gly        | TTC<br>Phe        | CGC<br>Arg<br>235 | CTG<br>Leu        | TCC<br>Ser        | TGG<br>Trp        | 722  |
| CCG<br>Pro<br>240 | CCC<br>Pro        | CTG<br>Leu        | CTG<br>Leu        | ACA<br>Thr        | GCG<br>Ala        | GAC<br>Asp<br>245 | TCT<br>Ser        | GGT<br>Gly        | TAC<br>Tyr        | TAC<br>Tyr        | GTG<br>Val<br>250 | CTG<br>Leu        | GAG<br>Glu        | TTG<br>Leu        | GTG<br>Val        | 770  |
| CCC<br>Pro<br>255 | AGT<br>Ser        | GGC<br>Gly        | AAA<br>Lys        | CTG<br>Leu        | GCA<br>Ala<br>260 | GCC<br>Ala        | ACA<br>Thr        | AGA<br>Arg        | CGC<br>Arg        | CAA<br>Gln<br>265 | CAG<br>Gln        | CTG<br>Leu        | CCC<br>Pro        | GGG<br>Gly        | AAT<br>Asn<br>270 | 818  |
| GCT<br>Ala        | ACC<br>Thr        | AGC<br>Ser        | TGG<br>Trp        | ACC<br>Thr<br>275 | TGG<br>Trp        | ACC<br>Thr        | GAC<br>Asp        | CTC<br>Leu        | AAC<br>Asn<br>280 | CCA<br>Pro        | GAC<br>Asp        | ACA<br>Thr        | GAT<br>Asp        | TAC<br>Tyr<br>285 | GAA<br>Glu        | 866  |
| GTA<br>Val        | TCG<br>Ser        | CTG<br>Leu        | TTG<br>Leu<br>290 | CCG<br>Pro        | GAG<br>Glu        | TCC<br>Ser        | AAT<br>Asn<br>295 | GTG<br>Val        | CGC<br>Arg        | CTC<br>Leu        | CTG<br>Leu        | AGG<br>Arg        | CCC<br>Pro<br>300 | CAG<br>Gln        | CAC<br>His        | 914  |
| TTG<br>Leu        | CGA<br>Arg        | GTA<br>Val<br>305 | CGC<br>Arg        | ACA<br>Thr        | CTG<br>Leu        | CAA<br>Gln        | GAG<br>Glu<br>310 | GAG<br>Glu        | GCA<br>Ala        | GGG<br>Gly        | CCA<br>Pro        | GAA<br>Glu<br>315 | CGC<br>Arg        | ATC<br>Ile        | GTC<br>Val        | 962  |
| ATC<br>Ile<br>320 | TCG<br>Ser        | CAT<br>His        | ACT<br>Thr        | AGG<br>Arg        | CCG<br>Pro        | CGC<br>Arg<br>325 | AGC<br>Ser        | CTC<br>Leu        | CGT<br>Arg        | GTA<br>Val        | AGT<br>Ser<br>330 | TGG<br>Trp        | GCC<br>Ala        | CCC<br>Pro        | GCA<br>Ala        | 1010 |
| CTT<br>Leu<br>335 | GGC<br>Gly        | CCG<br>Pro        | GAC<br>Asp        | TCC<br>Ser        | ACT<br>Thr<br>340 | CTC<br>Leu        | GGC<br>Gly        | TAC<br>Tyr        | CTT<br>Leu        | GTA<br>Val<br>345 | CAG<br>Gln        | CTC<br>Leu        | GGA<br>Gly        | CCT<br>Pro        | CTG<br>Leu<br>350 | 1058 |
| CAG<br>Gln        | GGC<br>Gly        | GGA<br>Gly        | TCC<br>Ser        | CTA<br>Leu<br>355 | GAA<br>Glu        | CAC<br>His        | GTG<br>Val        | GAG<br>Glu        | GTG<br>Val<br>360 | CCA<br>Pro        | GCT<br>Ala        | GGC<br>Gly        | CAG<br>Gln        | AAC<br>Asn<br>365 | AGC<br>Ser        | 1106 |
| ACT<br>Thr        | ACC<br>Thr        | ATC<br>Ile        | CAG<br>Gln<br>370 | GGC<br>Gly        | CTG<br>Leu        | ACG<br>Thr        | CCC<br>Pro        | TGC<br>Cys<br>375 | ACC<br>Thr        | ACT<br>Thr        | TAC<br>Tyr        | CTG<br>Leu        | GTG<br>Val<br>380 | ACT<br>Thr        | GTG<br>Val        | 1154 |
| ACT<br>Thr        | GCC<br>Ala        | GCC<br>Ala        | TTC<br>Phe<br>385 | CGC<br>Arg        | TCG<br>Ser        | GGC<br>Gly        | CGC<br>Arg<br>390 | CAG<br>Gln        | AGG<br>Arg        | GCG<br>Ala        | CTG<br>Leu        | TCG<br>Ser<br>395 | GCT<br>Ala        | AAG<br>Lys        | GCC<br>Ala        | 1202 |
| TGT<br>Cys        | ACG<br>Thr        | GCA<br>Ala        | TCT<br>Ser        | GGC<br>Gly        | GAG<br>Glu        | CGG<br>Arg        | ATC<br>Ile        | CGT<br>Arg        | GTC<br>Val        | CCG<br>Pro        | CAG<br>Gln        | GCC<br>Ala        | ATG<br>Met        | CGG<br>Arg        | CCG<br>Pro        | 1250 |



| 400                              | 405                               | 410 |      |
|----------------------------------|-----------------------------------|-----|------|
| GAG GCC GGA CTG CGG GAG CCC      | TGACCTTCCT GCCTCGTCCA CCCGAGGGGC  |     | 1301 |
| Glu Ala Gly Leu Arg Glu Pro      |                                   |     |      |
| 415                              | 420                               |     |      |
| CCTCTTCCTT AATCCAGTGA GAGAGGCACC | GCTGCTCGTG GTTTTCTTG TGGATGGAGT   |     | 1361 |
| GGGGTGGGGA GATGGGGGTG CTGGTCCTAC | CTTTGACCTG CGTAACTCCT CCGGTCGTTT  |     | 1421 |
| CCCCACTGGT CATCACCGCC CTTGCCTGAC | TCCCGGGA AA CCTGTAGCAA CCCTGGTAGC |     | 1481 |
| CTCACGCGCA ATGACAATCC TCTCCGGTTG | CCAGTGGAGT TGAGCACACG GTGGTCCTTG  |     | 1541 |
| GGCAACATTT GGCAGAGGGA TGGACAGTGT | TTGAGGTCAG GTTGAGACCC AGGAGAAGCA  |     | 1601 |
| TTCAGGAGAG GAGGCCACAG AGTTTCTAC  | CTGTGCCAAA GACTGGGCCC TCTGGTGGCA  |     | 1661 |
| AGGACTACAC ATGGCTTGGA GGAAATGTCC | AGGACCCTTC AAGTCCTGCC TGTGCCTAGA  |     | 1721 |
| AAGTGGGTAG GAGAAAGGGA GGAGAGAGTA | GTGTAGGCAA GGTTCCTCAA GACTTCCTTA  |     | 1781 |
| GGGCAAGGAA AGGTAGGGAG AGATACCGGG | AGGCTGATGA TGTTGCCAAC TAGTTTTCAT  |     | 1841 |
| CAAGATTTTC TGCCAGCCTG GAGGCCAGGA | TCTGTCAGGG TCACTGACTC TGCCTTCCTG  |     | 1901 |
| CCCAGGACCT GCACTGGGCC CCGCTATCAG | TGCGGGGGGG GGGGTGCAGA GTCTTCACAG  |     | 1961 |
| GAATGGGGGA TGAGACCTTG GCATGTAGTA | CATTGGGGAT AGGAGAGCCC TGCCGTGACA  |     | 2021 |
| GACTTACAGG GAGTCTCCTG CTTTAGTGTA | GGGAGCAAGG TGACATGCAG GTGGGCTACC  |     | 2081 |
| TCCTGTCATC ACTACTGCCC TGGGGCATCT | GACAGATACC TAAGGGTAGT CAGGAACAGG  |     | 2141 |
| CTTCCTCTCC AGTCCCTATG TACGCAGAGC | CCCTCCTCCC CAGAACCTCT TGCCCTAACC  |     | 2201 |
| TAAGCTTACT CCATCTCTCT TCCCCACTAA | TGACCCAGAC TCTAACAATA ATACAGTAAG  |     | 2261 |
| CCAGATGTAA ACTGTGAAGT CGAC       |                                   |     | 2285 |

## (2) INFORMATION FOR SEQ ID NO:56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Ala | Thr | Pro | Gly | Ala | Met | Leu | Phe | Trp | Thr | Val | Leu | Ser | Met | Ala |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Ser | Leu | Arg | Leu | Ala | Leu | Ala | Gln | Ser | Gly | Ile | Glu | Arg | Gly | Pro |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Thr | Ala | Ser | Ala | Pro | Gln | Gly | Asp | Leu | Leu | Phe | Leu | Leu | Asp | Ser | Ser |
|     |     | 35  |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| Ala | Ser | Val | Ser | His | Tyr | Glu | Phe | Ser | Arg | Val | Arg | Glu | Phe | Val | Gly |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

Gln Leu Val Ala Thr Met Pro Phe Gly Pro Gly Ala Leu Arg Ala Ser  
 65 70 75 80  
 Leu Val His Val Gly Ser Arg Pro His Thr Glu Phe Thr Phe Asp Gln  
 85 90 95  
 Tyr Ser Ser Gly Gln Ala Ile Gln Asp Ala Val Arg Val Ala Pro Gln  
 100 105 110  
 Arg Met Gly Asp Thr Asn Thr Gly Leu Ala Leu Ala Tyr Ala Lys Glu  
 115 120 125  
 Gln Leu Phe Ala Glu Glu Ala Gly Ala Arg Leu Gly Val Pro Lys Val  
 130 135 140  
 Leu Val Trp Val Thr Asp Gly Ala Ser Ser Asp Ser Val Gly Pro Pro  
 145 150 155 160  
 Met Gln Glu Leu Lys Asp Leu Gly Val Thr Ile Phe Ile Val Ser Thr  
 165 170 175  
 Gly Arg Gly Asn Leu Leu Glu Leu Leu Ala Ala Ala Ser Ala Pro Ala  
 180 185 190  
 Glu Lys His Leu His Phe Val Asp Val Asp Asp Leu Pro Ile Ile Ala  
 195 200 205  
 Arg Glu Leu Arg Gly Ala Ile Ile Asp Ala Met Gln Pro His Gln Leu  
 210 215 220  
 His Ala Ser Glu Ile Leu Ser Asn Gly Phe Arg Leu Ser Trp Pro Pro  
 225 230 235 240  
 Leu Leu Thr Ala Asp Ser Gly Tyr Tyr Val Leu Glu Leu Val Pro Ser  
 245 250 255  
 Gly Lys Leu Ala Ala Thr Arg Arg Gln Gln Leu Pro Gly Asn Ala Thr  
 260 265 270  
 Ser Trp Thr Trp Thr Asp Leu Asn Pro Asp Thr Asp Tyr Glu Val Ser  
 275 280 285  
 Leu Leu Pro Glu Ser Asn Val Arg Leu Leu Arg Pro Gln His Leu Arg  
 290 295 300  
 Val Arg Thr Leu Gln Glu Glu Ala Gly Pro Glu Arg Ile Val Ile Ser  
 305 310 315 320  
 His Thr Arg Pro Arg Ser Leu Arg Val Ser Trp Ala Pro Ala Leu Gly  
 325 330 335  
 Pro Asp Ser Thr Leu Gly Tyr Leu Val Gln Leu Gly Pro Leu Gln Gly  
 340 345 350  
 Gly Ser Leu Glu His Val Glu Val Pro Ala Gly Gln Asn Ser Thr Thr  
 355 360 365  
 Ile Gln Gly Leu Thr Pro Cys Thr Thr Tyr Leu Val Thr Val Thr Ala  
 370 375 380  
 Ala Phe Arg Ser Gly Arg Gln Arg Ala Leu Ser Ala Lys Ala Cys Thr  
 385 390 395 400

Ala Ser Gly Glu Arg Ile Arg Val Pro Gln Ala Met Arg Pro Glu Ala  
                             405                            410                            415

Gly Leu Arg Glu Pro  
                             420

## (2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2521 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: HW061

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 7..1422

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: complement (2089..2287)  
 (D) OTHER INFORMATION: /label= SAC\_24029

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

|                                                                                                                                                                                                                                       |     |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| GTCGAC GCG ACG GTG GCG GAG CAG TGG GTG CTG GTG GAG ATG GTG CAG<br>Ala Thr Val Ala Glu Gln Trp Val Leu Val Glu Met Val Gln<br>1                            5                            10                                             | 48  |
| GCG CTG TAC GAG GCT CCA GCA TAC CAT CTA ATT CTG GAA GGA ATC CTC<br>Ala Leu Tyr Glu Ala Pro Ala Tyr His Leu Ile Leu Glu Gly Ile Leu<br>15                            20                            25                            30    | 96  |
| ATA CTT TGG ATA ATC AGA CTC GTT TTC TCT AAA ACT TAC AAG TTG CAG<br>Ile Leu Trp Ile Ile Arg Leu Val Phe Ser Lys Thr Tyr Lys Leu Gln<br>35                            40                            45                                  | 144 |
| GAG CGT TCT GAC CTT ACA GCC AAG GAA AAG GAA GAA CTG ATT GAA GAA<br>Glu Arg Ser Asp Leu Thr Ala Lys Glu Lys Glu Glu Leu Ile Glu Glu<br>50                            55                            60                                  | 192 |
| TGG CAG CCA GAG CCC CTC GTC CCC CCG GTC TCC AGG AAC CAT CCT GCT<br>Trp Gln Pro Glu Pro Leu Val Pro Pro Val Ser Arg Asn His Pro Ala<br>65                            70                            75                                  | 240 |
| CTC AAC TAC AAC ATC GTC TCC GGC CCT CCA ACC CAT AAC ATC GTG GTG<br>Leu Asn Tyr Asn Ile Val Ser Gly Pro Pro Thr His Asn Ile Val Val<br>80                            85                            90                                  | 288 |
| AAC GGA AAA GAG TGT GTC AAC TTT GCC TCC TTT AAT TTC CTC GGG TTG<br>Asn Gly Lys Glu Cys Val Asn Phe Ala Ser Phe Asn Phe Leu Gly Leu<br>95                            100                            105                            110 | 336 |

|                   |            |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |      |
|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------|
| CTG<br>Leu        | GCC<br>Ala | AAC<br>Asn        | CCT<br>Pro        | CGG<br>Arg<br>115 | GTT<br>Val        | AAG<br>Lys        | GCT<br>Ala        | GCG<br>Ala<br>120 | GCT<br>Ala        | TTT<br>Phe        | GCA<br>Ala        | TCA<br>Ser        | TTA<br>Leu        | AAG<br>Lys<br>125 | AAG<br>Lys        | 384  |
| TAT<br>Tyr        | GGC<br>Gly | GTG<br>Val        | GGT<br>Gly<br>130 | ACC<br>Thr        | TGT<br>Cys        | GGT<br>Gly        | CCC<br>Pro        | AGA<br>Arg<br>135 | GGG<br>Gly        | TTT<br>Phe        | TAT<br>Tyr        | GGC<br>Gly        | ACA<br>Thr<br>140 | TTT<br>Phe        | GAT<br>Asp        | 432  |
| GTC<br>Val        | CAT<br>His | CTG<br>Leu<br>145 | GAT<br>Asp        | TTG<br>Leu        | GAA<br>Glu        | GAG<br>Glu        | CGC<br>Arg<br>150 | CTG<br>Leu        | GCA<br>Ala        | AAG<br>Lys        | TTT<br>Phe        | ATG<br>Met<br>155 | AAG<br>Lys        | ACC<br>Thr        | GAA<br>Glu        | 480  |
| GAA<br>Glu<br>160 | GCT<br>Ala | ATC<br>Ile        | ATT<br>Ile        | TAC<br>Tyr        | TCC<br>Ser        | TAT<br>Tyr<br>165 | GGC<br>Gly        | TTC<br>Phe        | TCC<br>Ser        | ACC<br>Thr        | ATA<br>Ile<br>170 | GCC<br>Ala        | AGT<br>Ser        | GCG<br>Ala        | ATT<br>Ile        | 528  |
| CCT<br>Pro<br>175 | GCG<br>Ala | TAC<br>Tyr        | TCT<br>Ser        | AAG<br>Lys        | AGA<br>Arg<br>180 | GGG<br>Gly        | GAC<br>Asp        | ATT<br>Ile        | GTT<br>Val        | TTT<br>Phe<br>185 | GTG<br>Val        | GAC<br>Asp        | AGT<br>Ser        | GCA<br>Ala        | GCC<br>Ala<br>190 | 576  |
| TGC<br>Cys        | TTT<br>Phe | GCT<br>Ala        | ATC<br>Ile        | CAG<br>Gln<br>195 | AAA<br>Lys        | GGA<br>Gly        | CTA<br>Leu        | CAG<br>Gln<br>200 | GCA<br>Ala        | TCA<br>Ser        | CGC<br>Arg        | AGT<br>Ser        | GAC<br>Asp        | ATT<br>Ile<br>205 | AAG<br>Lys        | 624  |
| TTA<br>Leu        | TTC<br>Phe | AAG<br>Lys        | CAC<br>His<br>210 | AAT<br>Asn        | GAC<br>Asp        | GTA<br>Val        | GCT<br>Ala        | GAC<br>Asp<br>215 | CTG<br>Leu        | GAG<br>Glu        | CGA<br>Arg        | CTG<br>Leu        | CTA<br>Leu<br>220 | AAA<br>Lys        | GAA<br>Glu        | 672  |
| CAA<br>Gln        | GAG<br>Glu | ATT<br>Ile<br>225 | GAA<br>Glu        | GAT<br>Asp        | CAA<br>Gln        | AAG<br>Lys        | AAT<br>Asn<br>230 | CCT<br>Pro        | CGA<br>Arg        | AAG<br>Lys        | GCC<br>Ala        | CGT<br>Arg<br>235 | GTG<br>Val        | ACT<br>Thr        | CGG<br>Arg        | 720  |
| CGA<br>Arg<br>240 | TTC<br>Phe | ATC<br>Ile        | GTC<br>Val        | GCG<br>Ala        | GAA<br>Glu        | GGA<br>Gly<br>245 | TTG<br>Leu        | TAT<br>Tyr        | ATG<br>Met        | AAC<br>Asn<br>250 | ACT<br>Thr        | GGA<br>Gly        | ACC<br>Thr        | ATC<br>Ile        | TGC<br>Cys        | 768  |
| CCT<br>Pro<br>255 | CTT<br>Leu | CCA<br>Pro        | GAA<br>Glu        | CTG<br>Leu        | GTG<br>Val<br>260 | AGG<br>Arg        | TTA<br>Leu        | AAG<br>Lys        | TAT<br>Tyr        | AAA<br>Lys<br>265 | TAC<br>Tyr        | AAA<br>Lys        | GCA<br>Ala        | AGG<br>Arg        | ATC<br>Ile<br>270 | 816  |
| TTC<br>Phe        | CTG<br>Leu | GAG<br>Glu        | GAG<br>Glu        | AGC<br>Ser<br>275 | CTG<br>Leu        | TCG<br>Ser        | TTC<br>Phe        | GGA<br>Gly        | GTC<br>Val<br>280 | CTT<br>Leu        | GGG<br>Gly        | GAG<br>Glu        | CAT<br>His        | GGG<br>Gly<br>285 | CGA<br>Arg        | 864  |
| GGA<br>Gly        | GTC<br>Val | ACC<br>Thr        | GAG<br>Glu<br>290 | CAC<br>His        | TAT<br>Tyr        | GGG<br>Gly        | ATC<br>Ile        | AGT<br>Ser<br>295 | ATT<br>Ile        | GAC<br>Asp        | GAC<br>Asp        | ATC<br>Ile        | GAC<br>Asp<br>300 | CTT<br>Leu        | ATC<br>Ile        | 912  |
| AGT<br>Ser        | GCT<br>Ala | AAC<br>Asn<br>305 | ATG<br>Met        | GAG<br>Glu        | AAT<br>Asn        | GCG<br>Ala        | CTC<br>Leu<br>310 | GCT<br>Ala        | TCT<br>Ser        | GTT<br>Val        | GGG<br>Gly<br>315 | GGC<br>Gly        | TTC<br>Phe        | TGC<br>Cys        | TGT<br>Cys        | 960  |
| GGC<br>Gly<br>320 | CGC<br>Arg | TCT<br>Ser        | TTC<br>Phe        | GTG<br>Val        | GTT<br>Val        | GAC<br>Asp<br>325 | CAT<br>His        | CAG<br>Gln        | CGG<br>Arg        | CTC<br>Leu        | TCT<br>Ser<br>330 | GGC<br>Gly        | CAA<br>Gln        | GGA<br>Gly        | TAC<br>Tyr        | 1008 |
| TGC<br>Cys<br>335 | TTT<br>Phe | TCA<br>Ser        | GCT<br>Ala        | TCA<br>Ser        | CTG<br>Leu<br>340 | CCC<br>Pro        | CCC<br>Pro        | CTG<br>Leu        | CTA<br>Leu        | GCC<br>Ala<br>345 | GCT<br>Ala        | GCC<br>Ala        | GCC<br>Ala        | ATT<br>Ile        | GAG<br>Glu<br>350 | 1056 |
| GCC<br>Ala        | CTC<br>Leu | AAC<br>Asn        | ATC<br>Ile        | ATG<br>Met<br>355 | GAG<br>Glu        | GAG<br>Glu        | AAC<br>Asn        | CCA<br>Pro        | GGG<br>Gly<br>360 | ATT<br>Ile        | TTT<br>Phe        | GCA<br>Ala        | GTT<br>Val        | TTA<br>Leu        | AAG<br>Lys<br>365 | 1104 |

|                                                                   |      |
|-------------------------------------------------------------------|------|
| AAA AAG TGC CAG ACC ATC CAC AAG TCC CTA CAA GGG GTT TCC GGT TTA   | 1152 |
| Lys Lys Cys Gln Thr Ile His Lys Ser Leu Gln Gly Val Ser Gly Leu   |      |
| 370 375 380                                                       |      |
| AAA GTG GTG GGG GAG TCC CTT TGC CCA GCG CTT CAC CTC CAG CTG GAA   | 1200 |
| Lys Val Val Gly Glu Ser Leu Cys Pro Ala Leu His Leu Gln Leu Glu   |      |
| 385 390 395                                                       |      |
| GAG AGC ACG GGC TCT CGG GAG AGA GAT ATG AAG CTG CTT CAG GAG ATT   | 1248 |
| Glu Ser Thr Gly Ser Arg Glu Arg Asp Met Lys Leu Leu Gln Glu Ile   |      |
| 400 405 410                                                       |      |
| GTA GAG CAA TGC ATG AAT AAG GGC ATC GCA TTG ACT CAG GCA CGC TAC   | 1296 |
| Val Glu Gln Cys Met Asn Lys Gly Ile Ala Leu Thr Gln Ala Arg Tyr   |      |
| 415 420 425 430                                                   |      |
| TTG GAC AAG GAA GAG AAG TGC CTT CCT CCT CCA AGC ATC AGG GTT GTG   | 1344 |
| Leu Asp Lys Glu Glu Lys Cys Leu Pro Pro Pro Ser Ile Arg Val Val   |      |
| 435 440 445                                                       |      |
| GTC ACC GTG GAG CAG ACA GAC GAA GAG CTG CAG AGG GCT GCA GCC ACC   | 1392 |
| Val Thr Val Glu Gln Thr Asp Glu Glu Leu Gln Arg Ala Ala Ala Thr   |      |
| 450 455 460                                                       |      |
| ATC AGG GAG GCG GCC CAG GCT GTG CTT TTG TAGGCTCCTG CCCAGTGCTT     | 1442 |
| Ile Arg Glu Ala Ala Gln Ala Val Leu Leu                           |      |
| 465 470                                                           |      |
| GCGACCATGT CACCTGCAGA CAGAACTACT CAGACCTCCA GCTGCCCAGG GCGTGGAGTG | 1502 |
| CTGCCCAGGG CGTGGCTGCC CTTGAGTCCA CAGCCAGAAT GGATGGCTTT ACCCAGCAGG | 1562 |
| CTTCCAGAGG ATGGCAGACG ACGGTGTAAC ACTGGTGTTT ATGCGGTGCC ATGGCTCTGT | 1622 |
| CTCTTATACT CGCCTTTGTT TAAAACTGGA GCTTCCGTTT TCCCTCTCCC GCCTGTGGGA | 1682 |
| ACAATTCGAT AAGCACTCCT CTGTATTCCA TACAAAAGGA CTTGCAGCTG AGAGGAAGTC | 1742 |
| TCCACGCACC ACAGTTACTG TGGGATGATA GACTGTGGCC TCCCAGGTCC TTCGGGTAGA | 1802 |
| GCTCAGTGGT GGCTGCTGTG CAGACAACTC CTGTGTGTCA AACTGTCTAT AGAACATGTT | 1862 |
| GATCCTAGAA CTCTGTGTGC TCCAGTTACT GATGCTGTGC TGTCTAATCT GAGCTTCACT | 1922 |
| AACAATAGTC ATACCGCTCC CTAAGCAATA ATCTGAATCA AACATTATTT TATTTTGTG  | 1982 |
| TAATTGACTT TATATTTTTT ATATATTCTC TAGTCAGTTT TGGGAAGAGG GTTATTATTC | 2042 |
| TGGTCCCCAA ATATATAAAT CATATCCTTG GTATTTTTTA ATATGTACGG TGTCCTTTTT | 2102 |
| CATGGTGGTT TTGTCCAGGA ACATAGAAGT GTGGGCCTTT TCTAAGCTGA GAAAAGAGAG | 2162 |
| AACTTTCCTC TTTCGTCTA TAAATCCAG ATGCCTCAGA AAATAGGAAT GCTCTGAAAA   | 2222 |
| CTGCTGCTGT CCTTAGCGAG CGTGCTGAGG GGTGTAACGG CTTGTGACAT GTGCCGCGAT | 2282 |
| CGTGACATG GAAGGCCATT ACTCCCTCTC GCTGCACAGG CAGAGGAATG GGGCCTCTAA  | 2342 |
| CCGTCGTTTT CGGATGTTCA TTCATGTTAA CAGTGGACGG CATCTTCCTA AGTGATCTGT | 2402 |
| GACATGTTTA ATGTGTCTAT TTCATACGTG CCTTGTGAAT GCTGCTGCTG TGAGGGTACG | 2462 |

GGGATGAGTC TGTTTTGGTT TGGTTTTTAA TGAAATAAAC CTCCAAGAGC CTACAAAAA 2521

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Thr | Val | Ala | Glu | Gln | Trp | Val | Leu | Val | Glu | Met | Val | Gln | Ala | Leu | 1   | 5   | 10  | 15  |
| Tyr | Glu | Ala | Pro | Ala | Tyr | His | Leu | Ile | Leu | Glu | Gly | Ile | Leu | Ile | Leu | 20  | 25  | 30  |     |
| Trp | Ile | Ile | Arg | Leu | Val | Phe | Ser | Lys | Thr | Tyr | Lys | Leu | Gln | Glu | Arg | 35  | 40  | 45  |     |
| Ser | Asp | Leu | Thr | Ala | Lys | Glu | Lys | Glu | Glu | Leu | Ile | Glu | Glu | Trp | Gln | 50  | 55  | 60  |     |
| Pro | Glu | Pro | Leu | Val | Pro | Pro | Val | Ser | Arg | Asn | His | Pro | Ala | Leu | Asn | 65  | 70  | 75  | 80  |
| Tyr | Asn | Ile | Val | Ser | Gly | Pro | Pro | Thr | His | Asn | Ile | Val | Val | Asn | Gly | 85  | 90  | 95  |     |
| Lys | Glu | Cys | Val | Asn | Phe | Ala | Ser | Phe | Asn | Phe | Leu | Gly | Leu | Leu | Ala | 100 | 105 | 110 |     |
| Asn | Pro | Arg | Val | Lys | Ala | Ala | Ala | Phe | Ala | Ser | Leu | Lys | Lys | Tyr | Gly | 115 | 120 | 125 |     |
| Val | Gly | Thr | Cys | Gly | Pro | Arg | Gly | Phe | Tyr | Gly | Thr | Phe | Asp | Val | His | 130 | 135 | 140 |     |
| Leu | Asp | Leu | Glu | Glu | Arg | Leu | Ala | Lys | Phe | Met | Lys | Thr | Glu | Glu | Ala | 145 | 150 | 155 | 160 |
| Ile | Ile | Tyr | Ser | Tyr | Gly | Phe | Ser | Thr | Ile | Ala | Ser | Ala | Ile | Pro | Ala | 165 | 170 | 175 |     |
| Tyr | Ser | Lys | Arg | Gly | Asp | Ile | Val | Phe | Val | Asp | Ser | Ala | Ala | Cys | Phe | 180 | 185 | 190 |     |
| Ala | Ile | Gln | Lys | Gly | Leu | Gln | Ala | Ser | Arg | Ser | Asp | Ile | Lys | Leu | Phe | 195 | 200 | 205 |     |
| Lys | His | Asn | Asp | Val | Ala | Asp | Leu | Glu | Arg | Leu | Leu | Lys | Glu | Gln | Glu | 210 | 215 | 220 |     |
| Ile | Glu | Asp | Gln | Lys | Asn | Pro | Arg | Lys | Ala | Arg | Val | Thr | Arg | Arg | Phe | 225 | 230 | 235 | 240 |
| Ile | Val | Ala | Glu | Gly | Leu | Tyr | Met | Asn | Thr | Gly | Thr | Ile | Cys | Pro | Leu | 245 | 250 | 255 |     |
| Pro | Glu | Leu | Val | Arg | Leu | Lys | Tyr | Lys | Tyr | Lys | Ala | Arg | Ile | Phe | Leu |     |     |     |     |

| 260 |     |     |     |     |     |     | 265 |     |     |     |     |     |     | 270 |     |  |  |  |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|
| Glu | Glu | Ser | Leu | Ser | Phe | Gly | Val | Leu | Gly | Glu | His | Gly | Arg | Gly | Val |  |  |  |  |  |
| 275 |     |     |     |     |     |     | 280 |     |     |     |     |     |     | 285 |     |  |  |  |  |  |
| Thr | Glu | His | Tyr | Gly | Ile | Ser | Ile | Asp | Asp | Ile | Asp | Leu | Ile | Ser | Ala |  |  |  |  |  |
| 290 |     |     |     |     |     |     | 295 |     |     |     |     |     |     | 300 |     |  |  |  |  |  |
| Asn | Met | Glu | Asn | Ala | Leu | Ala | Ser | Val | Gly | Gly | Phe | Cys | Cys | Gly | Arg |  |  |  |  |  |
| 305 |     |     |     |     |     |     | 310 |     |     |     |     |     |     | 315 |     |  |  |  |  |  |
| Ser | Phe | Val | Val | Asp | His | Gln | Arg | Leu | Ser | Gly | Gln | Gly | Tyr | Cys | Phe |  |  |  |  |  |
| 320 |     |     |     |     |     |     | 325 |     |     |     |     |     |     | 330 |     |  |  |  |  |  |
| Ser | Ala | Ser | Leu | Pro | Pro | Leu | Leu | Ala | Ala | Ala | Ala | Ile | Glu | Ala | Leu |  |  |  |  |  |
| 335 |     |     |     |     |     |     | 340 |     |     |     |     |     |     | 345 |     |  |  |  |  |  |
| Asn | Ile | Met | Glu | Glu | Asn | Pro | Gly | Ile | Phe | Ala | Val | Leu | Lys | Lys | Lys |  |  |  |  |  |
| 350 |     |     |     |     |     |     | 355 |     |     |     |     |     |     | 360 |     |  |  |  |  |  |
| Cys | Gln | Thr | Ile | His | Lys | Ser | Leu | Gln | Gly | Val | Ser | Gly | Leu | Lys | Val |  |  |  |  |  |
| 365 |     |     |     |     |     |     | 370 |     |     |     |     |     |     | 375 |     |  |  |  |  |  |
| Val | Gly | Glu | Ser | Leu | Cys | Pro | Ala | Leu | His | Leu | Gln | Leu | Glu | Glu | Ser |  |  |  |  |  |
| 380 |     |     |     |     |     |     | 385 |     |     |     |     |     |     | 390 |     |  |  |  |  |  |
| Thr | Gly | Ser | Arg | Glu | Arg | Asp | Met | Lys | Leu | Leu | Gln | Glu | Ile | Val | Glu |  |  |  |  |  |
| 395 |     |     |     |     |     |     | 400 |     |     |     |     |     |     | 405 |     |  |  |  |  |  |
| Gln | Cys | Met | Asn | Lys | Gly | Ile | Ala | Leu | Thr | Gln | Ala | Arg | Tyr | Leu | Asp |  |  |  |  |  |
| 410 |     |     |     |     |     |     | 415 |     |     |     |     |     |     | 420 |     |  |  |  |  |  |
| Lys | Glu | Glu | Lys | Cys | Leu | Pro | Pro | Pro | Ser | Ile | Arg | Val | Val | Val | Thr |  |  |  |  |  |
| 425 |     |     |     |     |     |     | 430 |     |     |     |     |     |     | 435 |     |  |  |  |  |  |
| Val | Glu | Gln | Thr | Asp | Glu | Glu | Leu | Gln | Arg | Ala | Ala | Ala | Thr | Ile | Arg |  |  |  |  |  |
| 440 |     |     |     |     |     |     | 445 |     |     |     |     |     |     | 450 |     |  |  |  |  |  |
| Glu | Ala | Ala | Gln | Ala | Val | Leu | Leu |     |     |     |     |     |     |     |     |  |  |  |  |  |
| 455 |     |     |     |     |     |     | 460 |     |     |     |     |     |     | 465 |     |  |  |  |  |  |
| 470 |     |     |     |     |     |     | 475 |     |     |     |     |     |     | 480 |     |  |  |  |  |  |

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW062

(ix) **FEATURE:**

- (A) NAME/KEY: misc\_feature  
(B) LOCATION: complement (87..223)  
(D) OTHER INFORMATION: /label= SAC 24443

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```

TTTTTGTGAG CAAATCCAAA TTTATTTTAA TGCCATGTCA TTTCAAAAAC CCCAGCCTTG 60
GTTCCCTGGA ACAGCATGCC AGAGGTACAA AGTGTAACCT TCCTCTATAA ACCCCCAGCA 120
AGTCATCCAA GTCCTCAGCT TCAGAAAGTC AGTTCTCTTC AGTCTACTCC TCTGGTTCCT 180
GGTTTTTCTT TCAAGGAAGG CAACTTAAAA ATTAGGTAGC TGAGGTTCCA ATGTTGGTGG 240
CTAACCTTGC CTCCTCTTTT GTTCTGTAGT AGGGCCACAA ACCTTGACCA GGCAGAGTAG 300
TAGAAAAGTA GAAAGAGGGG CTTGACGACG GTGGATTTTG ACTCCTGATT TTATTATTCA 360
ATTTCTTTTT CTACTAAAAG TAGTCTTCGG TGGTTGGGAA GCCTGGCCTC CCAACACCAG 420
AGTCAGTCGG AGCTGGTTTT TTTGTTGAAA GGAGTGGGCG GGTGGGTGGG GGACCGGGAT 480
GAGGGCAGAA CCCCGCTCTG CTGGTAGTCT TGGGTGGAGA AGACGAACTG CACTTGACAG 540
AGCCTGGGGG TCGGGTGGGA GGGGGTGAGG CAGGAGTGAC AGCTGGGGAG GGGACCCA 598

```

## (2) INFORMATION FOR SEQ ID NO:60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (vii) IMMEDIATE SOURCE:

(B) CLONE: HW066

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 759..906
- (D) OTHER INFORMATION: /label= SAC\_24521

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```

ATTCGCGGCC GGCTCGACTT TTTTTTTTGT GATATAAAAA ATTTATTTTA GAAATCACAT 60
CTTTAAAAAA CAACATAGAA GGTATCCTG ACCAGATATA AATTCTTCAT TCAATGCCAG 120
GGTGTATGT GGTACAATTA GCGGGATGTT CTGTGAGGAG AATGAGCTG TGTGATACTC 180
TCGACATGTA CACCAGCTCA AACGTTAATG CGGCTTTTAA AAGGAAGGAG AGAGGAAGGC 240
AGCGAGAGAG GAGGAAACTG TTTTGGAAC AGAAGAGCAT CTCCGTCCTG CACCTGTCAG 300
CCCTGAAACT CCCGGCCCTT GAGACCAGCC CAGCAGAGGC TGCACGAANN NGCATCATTT 360
TAATTCACAA GTGACTGCAG CACCCTGGCA TCTTGTGCTG GGAGTGTGGG TGGGAACAGA 420

```



|                                                                    |      |
|--------------------------------------------------------------------|------|
| GGTGACAAGT CTGCTCTGTA GTGTCATAGC CAGAGAGCAA CAGGGACTCT AGAGGAAGAA  | 480  |
| GAGCAAAGCT TGCCTAGACA GAACGGGTTG TCCCTGTCCC TGTCCATCAG CTTTCTTATA  | 540  |
| ACCTATGGNT AGCCAGGATC AAATACCTGA AAGTCAGAAT GTAAAAATAA AGTGTCAAGT  | 600  |
| AACACTTATT GCGGACAGAA ATACAGCTCT TTACGCCTAC AACCATAAAC CCAGTGGTGA  | 660  |
| GGCTGGGACA GACCTTTTAT GCCGAAGTTC TCACAACTCG GGACTGACTT ACTGGGGCCT  | 720  |
| GGTCACTGCT TAATTGGTGA CCTCACACCA TTTCAGGTAC TTCTGCCCAG CTCCTGATTC  | 780  |
| CTCTTCAGGA GAAACAGGAA GCAGACTTTG TTAGTAAGTG GGTCAATGCAG GGCTGGGCCG | 840  |
| CCTACATGGG ACTTAACACA GAGAGAATAC TGCCAGCTTC CCAAACACTT CAAGAGAGAA  | 900  |
| AAATGTCCAG ACGTGGGTGC TGCAGCAACC TTCCAAGAGT GAGGCCCCCTG CACCCCTCTG | 960  |
| CACCCCTCGC TGGGGACAGT GGGCTCTGGT GGCTTGAAC T GAGTAGATCG GATCATTTCC | 1020 |
| TCCTCTTTCT GAGACAAGGC TTCACGTGTG AGCCCNNGCT GCCCTGGAGC TCACTATTTA  | 1080 |
| GACCAGGCTA GGATCTCACA GAGAACCACC TGCCCTCTGGC CTCTCAAGAG CTGGGATTAA | 1140 |
| GGTGTGAAAA GGGGGCTAAT GTAGCCCAGG CTGGCTCCTG CTCCACAGGG CTTCAGGGC   | 1200 |
| AGTTCTGGAT CCTACCAGCA AGTACAAGCT GGTACCCAGA GGACGCTGCA GGATGGAAGG  | 1260 |
| ACGGAAGGCC AGGAGCCTTC GTTTGATTTG ACGGGAAGGA GGAGGAACAG TGAGGTTGTG  | 1320 |
| CATCTGAGCT TTATTACCAG GACGATGATG TCACCTCAGG AAGGGACTGG GATCCCTGCA  | 1380 |
| AGTGGTTCCA CATGGGACCC AGGTCTCAG AGATGTGGCC CTCCTGTGTG GCCAAATGC    | 1440 |
| ATCTGGAAAG AAAATACAGA AGGGGAGGGA CAGCATAGGA GGAGACAAGT GTGACCCGAG  | 1500 |
| GCCCAGGAAG TACTTCCATA TTCTGTCTCT CTCCAGGCAC GAGAGTTGAA GGCCGTGCCA  | 1560 |
| AGCCCTGCAC TCGCTAAGCT GGTGAAGACC ACACCAAAT CACTGTGACA GGACAGCTGC   | 1620 |
| ACAGATCTGT TTCCGACTTT TCCCACCAG ATTCTACACC AAGGTAAAAA AGAGCTTCCA   | 1680 |
| CCACAAATCC AAGGCAGGAG CTGGGCGGCC ACACACCCGC CACAGATGGT GCAAGTTGCT  | 1740 |
| CACTTCCGCA GCCGGTGGCA GGACAGGGAG GAGGGCAGAG TCCTGAGACA AGAACCCAG   | 1800 |
| AGCGGGGCCA GTTCAGTCAG TGGTGGACCT CCGGTACCAG AACCGAGCTC GGAAGTCGTC  | 1860 |
| GCTGCACGTC ATGAAGCCAG GGTGGTGGG GAGTGCAGT ATGCAGCGCA CAATGTTGTT    | 1920 |
| GTGGCCCAGG GACAGCAGGT TCCTGCGCTC AGCTGTCTTA GAGTCCCAGC AGCACAGGCT  | 1980 |
| GATGGTCTTT TCGTCCGCA GCAAAATATA GTCCTCAGTG TGGTTGAACA CAGCCTGTGT   | 2040 |
| CCGGGTGCAC TTGCCGTCCA CTCAGCCCTG CGCCTGTGTA CCTCACCAGT GTCCGTCCCG  | 2100 |
| TGGATATTTT CCCAGAGTTT AGCTACAGAG TCTTTTCCNN GAGTTTAGGC CTACAGAGTC  | 2160 |
| TTTTCCACTT GAGAGGATGT ACTTGAATT CTTGGAGAAA ATGGCAGAAC AGACTTCTGC   | 2220 |
| CCCGTCGTGA GCTTTCTCAA AGGTTGTGAT GCAGCGATTG GAGACGCCGT CCCACAGCTT  | 2280 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GATGCAGCCG TCCTTGCTGC CAGTGACATA CATGTTGGCA CTAGGGTTAT AGTTGACAGA  | 2340 |
| GCAGATGGCG TCGGTGTGCT GGTCTTGGGG ATTGCAGGAG ACGAAACACT GGAAGGTGTT  | 2400 |
| GATGTCATAG AGGCGAAGCG TGGGATGCTG GGTCCCGACC AGGATGAAGT CTCCAGAAGG  | 2460 |
| GTGGAACGAG ATGGAGCGCA GCATCTCAGC TTCCTGAATG TATTTAAAGG CTCTTTTTGC  | 2520 |
| AGAGGGTTTG GAATAATCAA ACAATTTTAG AGTATAATCC CTTGAGCCGG AGGCCAGGAT  | 2580 |
| CTGTTCTGTT GGGTGAAAAG CGAGACACGT GACTTCATCC ACATGGTCGT AAAGAGTTCG  | 2640 |
| GATCACTGGG TGTTCTCCA TGTTCTGTTG TGCAGTCTCA TTCATCATGA CCCTCGATGG   | 2700 |
| GCATGGCGCT CTTGGCCAGC ATCCTCTCTG TGTCCAGTAT CTTGATGGAA GCATCCGCAG  | 2760 |
| ACCTGTGGC TATCAACTGC CCATCTCTGC TGTAGGTGGC CACTCGGCAT GGGCCTTTGT   | 2820 |
| GGGAGGTGAC ATAACAGGTT TCATACTCCG AAGCCTCGGG TGACATTGTT TGGACGCTG   | 2880 |
| CATCAAACTC CAGGTCAATN CTGTGCCAGG GGCAACCGTG TCAGAGCGAC CAATGGCATA  | 2940 |
| CTGAACTGCA GTGTCATCGT TCTCCATCCC TAGCTTGATG AGGTGCAGGA GCTGCTCCGA  | 3000 |
| GGGCGCACAC ACCGACTGTG GCTTGATCTC GTTGATGAGG CCATTGCGAT GCTAATGTAT  | 3060 |
| CCGTCATAGA GCAGCTGGCT GATGATCAGC TTGTAGAGCT GCTGGCGGTC CTTCAGGCCC  | 3120 |
| ACTTTGGTTC TGTACATTCT GCACAAGAGG ATGACAGTTC CCCTGACTTC TCCGAGCTGA  | 3180 |
| TCACCTCCGC GACAGCCTTG AATCCAAAGG ACTGTGAGTG ACCGGCAAAC GCCCGAN CCT | 3240 |
| TGGAGAGCAC NGCGGGCGAT AGAACGGCCG TAGATCGGAC AGGCCGTTGG TGCACCGTCG  | 3300 |
| ACCGG                                                              | 3305 |

## (2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2099 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: HW069
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1360..1893
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 1744..1885
  - (D) OTHER INFORMATION: /label= SAC\_24477
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GTGACGCAT CCAGGCAGGC ATGGAGCAGG TAGGGCTCAG AGTTCTACAT CTTTCATCTGG  | 60   |
| AGGCTACTAT GAGGAGACCG ACTTCCAGGC AGCTAGGAAG CCCATGCTCA CAGTGACAGA  | 120  |
| CCTTCTCCAA CAAGGTTATA CCTCCTAATC GTGCCGCTCC CTGGGCCAAG CATATGCAAA  | 180  |
| CCTTCACACA GGTCTTCCTC CTACACAGTG GGGCTTCTGG GCCCCACTCA CGGCCAGTAC  | 240  |
| ATGGCAAAAG ACATTAAAGA TGCAC TTGGA CCAGCTCAGG GCCCTGTTCT GCAGCCAGGT | 300  |
| ATCATGGATG GAGGAAGTCC TGA CTGAAAC AAAAATGTCT GTCCGCATTG TCATCTTTGA | 360  |
| GAGCCTGAAC AAACCCCGAA CACCTCTGAC CTGGCACAGG GACCCTGAGT CTGCCTGCCT  | 420  |
| GGCACTCTGA ACTTGCTGGC TACTGGGCTG AAGTCTCAGG ATCGAGGTAC AAGGACAAAG  | 480  |
| CCTGTTGGTA TTATGTAGAC AGGAGCCCCA GGGGGCTCAG AGCAGGGGTT TACCGTTACT  | 540  |
| CTTGGTCCAG CCGGCACAGT GGTCTTCCCT CAGTTTTTGT TTTTGT TTTT TTGTTTTTTT | 600  |
| GTTTTGT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT               | 660  |
| CCTGCAGTCT GGACTGCCCC CTTGGGCAAT ACATTTTGAT GGAAACCAAC TTCTGTGTTC  | 720  |
| CCAGATCGGC AGCCTCTCCA TGCCGAGCAC CCCTGTTCTA GCTAACCCGG ACATGCTACA  | 780  |
| CCCCTGCCGT GGTGGTTCA TCTCCCCACT CCCCGCCGTG TCTTAATAAC ACGGTGGATG   | 840  |
| GATGGACAGA CGGACAGATG AAGCTTTGAC AGCTAGCCAC TGCTCTGCTC CTTTCTCTTT  | 900  |
| GTCTTCTGAG TAAATCTCA AACTCAAGCC TCCCAGGGGG AGCCCAGAAC CCCACCCACC   | 960  |
| ACTAGTGAAA AAGCAGCTTT TTAGGCAGCT CAGAGAGTGT CCGGAGCAGG GTTCCTACAG  | 1020 |
| GCTCAGGTTG GGGGCAGTTT CAGTGTGTGG CTGCCGGCCC AGGGCCCTCC CTGGTCAGCA  | 1080 |
| CCTAGGTAGA GAGGAAGCAG GAAGGACCAA GTCCAGCTCA AAGGAACCAG TGAGGCTGGT  | 1140 |
| TGAGAGCAGA CGGTGGGTAT GGGTCTGTGA AAAGAAAAGT AGGCCGTTGG GAGCCCACCG  | 1200 |
| GAGGACAGTC TGGCTCAAGG CATCACACCT GGTTCAGCA GCCTCCGAGA CAGCAGCCCCG  | 1260 |
| TGGGTGTGAA CTTGGCTCCA TCTTGCTGA ATTCTGCTGC CCCAGAGAAG AATCTGGCAC   | 1320 |
| CGGAGTGGAC CCAGATACGT GTCACAGCCT TGGAAATCG ATG GCA GCG AGA CCC     | 1374 |
| Met Ala Ala Arg Pro                                                |      |
| 1 5                                                                |      |
| TTT ATT GGG CAC CTA GAG ATT TCC GAG AGG CGG TTC CTA ACA TTG TCA    | 1422 |
| Phe Ile Gly His Leu Glu Ile Ser Glu Arg Phe Leu Thr Leu Ser        |      |
| 10 15 20                                                           |      |
| TTC CTT TCC CAC AGG CCT CAG GTC CAG GCC CAA AGC CAA GTG ACT GCC    | 1470 |
| Phe Leu Ser His Arg Pro Gln Val Gln Ala Gln Ser Gln Val Thr Ala    |      |
| 25 30 35                                                           |      |
| CTC ATC GGC TCA GCA CAT CGG CGG GTG CTG GAT GTG CCG CCT GCA GAG    | 1518 |
| Leu Ile Gly Ser Ala His Arg Arg Val Leu Asp Val Pro Pro Ala Glu    |      |
| 40 45 50                                                           |      |
| GCT CTT CGG GGC CAG GCT GGG ACT GGG CCC CTG AGA AAA CCC AAA CTC    | 1566 |
| Ala Leu Arg Gly Gln Ala Gly Thr Gly Pro Leu Arg Lys Pro Lys Leu    |      |

|                                                                                                                                                       |      |    |  |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|----|--|
| 55                                                                                                                                                    | 60   | 65 |  |
| TGT GCC TTA CCC AGT CAG GAT CCT TGG GAG CCT TGG CCC TCG ATG CCA<br>Cys Ala Leu Pro Ser Gln Asp Pro Trp Glu Pro Trp Pro Ser Met Pro<br>70 75 80 85     | 1614 |    |  |
| GGA CCT GGC CTA GCA TCA CCC TGG GCC ACC TGC ACG TTC ATG GCC TCA<br>Gly Pro Gly Leu Ala Ser Pro Trp Ala Thr Cys Thr Phe Met Ala Ser<br>90 95 100       | 1662 |    |  |
| CCA TCT GCT TTG CGA ACC ACT ACC CAC CCC CTG TCG CAT GCA CCT TCC<br>Pro Ser Ala Leu Arg Thr Thr His Pro Leu Ser His Ala Pro Ser<br>105 110 115         | 1710 |    |  |
| ACC CCT GCG GTG TCT GAC TCT AGG GAG ATA GGT ACA GAT GTC TGT GAT<br>Thr Pro Ala Val Ser Asp Ser Arg Glu Ile Gly Thr Asp Val Cys Asp<br>120 125 130     | 1758 |    |  |
| GGG CTG AGA CAT CCC CCA CCC CCC ACG GCT CAT TGG TTT CTT TTA GCT<br>Gly Leu Arg His Pro Pro Pro Thr Ala His Trp Phe Leu Leu Ala<br>135 140 145         | 1806 |    |  |
| GAG TGC TGT TTT CTG TGT CTT TAC TCT GCT ATG ATG ACT TGG GGG GTT<br>Glu Cys Cys Phe Leu Cys Leu Tyr Ser Ala Met Met Thr Trp Gly Val<br>150 155 160 165 | 1854 |    |  |
| AGT GAG GGC CTG AGG GAT GCT TGT TGG AAG TAC TGT GGG TAGGGCCTGG<br>Ser Glu Gly Leu Arg Asp Ala Cys Trp Lys Tyr Cys Gly<br>170 175                      | 1903 |    |  |
| TAGGTCCTTA GGGAACAAAC AAACAAAAGG CTCATCTGCT CCTGGGTGGT GACCTGGCCA                                                                                     | 1963 |    |  |
| CAGCACCTGT CATCTCCCTT GGTGTCTGCC CAGTGGGGAC GAGCTTCCCT GGCTCAACCC                                                                                     | 2023 |    |  |
| CTATCAGGTG TGCACTGTTG AGTCTGCGGG CCAGCCGGGA CTTTAACCAA TAAAGAGCAA                                                                                     | 2083 |    |  |
| CCTTGCTGTGT CAAAAA                                                                                                                                    | 2099 |    |  |

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met Ala Ala Arg Pro Phe Ile Gly His Leu Glu Ile Ser Glu Arg Arg  
1 5 10 15

Phe Leu Thr Leu Ser Phe Leu Ser His Arg Pro Gln Val Gln Ala Gln  
20 25 30

Ser Gln Val Thr Ala Leu Ile Gly Ser Ala His Arg Arg Val Leu Asp  
35 40 45

Val Pro Pro Ala Glu Ala Leu Arg Gly Gln Ala Gly Thr Gly Pro Leu  
50 55 60

Arg Lys Pro Lys Leu Cys Ala Leu Pro Ser Gln Asp Pro Trp Glu Pro

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 65  |     | 70  |     | 75  |     | 80  |     |     |     |     |     |     |     |     |     |
| Trp | Pro | Ser | Met | Pro | Gly | Pro | Gly | Leu | Ala | Ser | Pro | Trp | Ala | Thr | Cys |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Thr | Phe | Met | Ala | Ser | Pro | Ser | Ala | Leu | Arg | Thr | Thr | Thr | His | Pro | Leu |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Ser | His | Ala | Pro | Ser | Thr | Pro | Ala | Val | Ser | Asp | Ser | Arg | Glu | Ile | Gly |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |
| Thr | Asp | Val | Cys | Asp | Gly | Leu | Arg | His | Pro | Pro | Pro | Pro | Thr | Ala | His |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Trp | Phe | Leu | Leu | Ala | Glu | Cys | Cys | Phe | Leu | Cys | Leu | Tyr | Ser | Ala | Met |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |
| Met | Thr | Trp | Gly | Val | Ser | Glu | Gly | Leu | Arg | Asp | Ala | Cys | Trp | Lys | Tyr |
|     |     |     | 165 |     |     |     |     | 170 |     |     |     |     |     | 175 |     |

Cys Gly

## (2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1210 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: HW070
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: complement (639..928)
  - (D) OTHER INFORMATION: /label= SAC\_24286
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

|            |            |            |            |            |            |     |
|------------|------------|------------|------------|------------|------------|-----|
| GTCGACGCAG | ATTTTGATGG | CGTCCTTTAT | CATATTTCAA | ATCCTAATGG | AGACAAAACA | 60  |
| AAAGTGATGG | TCAGTATTTT | TTTGAAATTC | TACAAGGAAC | TTCAGGCACA | CGGAGCTGAT | 120 |
| GAGTTACTAA | AGAGAGTATA | CGGAAGTTTC | TTGGTGAACC | CAGAATCAGG | ATACAATGTG | 180 |
| TCTTTGCTAT | ATGACCTGGA | AAATCTACCT | GCATCCAAGG | ATTCTATTGT | GCATCAGGCT | 240 |
| GGCATGTTGA | AGCGAAATTG | TTTTCCTCT  | GTGTTTGAGA | AATACTTCCA | ATTCCAAGAA | 300 |
| GAGGGCAAAG | AAGGAGAGAA | CAGAGCAGTT | ATCCATTATA | GAGATGATGA | GACCATGTAT | 360 |
| GTGGAATCTA | AAAAAGACAG | AGTCACAGTA | GTCTTCAGCA | CAGTTTTTAA | GGATGACGAC | 420 |

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GATGTGGTCA TTGGAAAGGT GTTCATGCAG GAGTTCAAAG AAGGACGAAG AGCCAGCCAC 480
ACAGCCCCCC AGGTCCTTTT TAGCCACAGG GAACCTCCTC TAGAACTGAA AGACACAGAT 540
GCTGCCGTGG GTGACAACAT TGGCTACATC ACCTTTGTGC TGTTCCTCG CCACACCAAT 600
GCCACTGCTC GAGACAACAC CATCAACCTG ATCCACACGT TCCGGGACTA TCTGCACTAC 660
CACATTAAGT GCTCTAAGGC CTATATTCAT ACACGAATGC GAGCAAAAAC ATCCGACTTC 720
CTTAAGGTGC TCAACCGTGC ACGCCCAGAT GCCGAGAAAA AAGAAATGAA AACAAATCACG 780
GGGAAGACTT TTTTCATCCCG CTAATCTTG GGAAGTGGG AGGAAGCACT GTTGACCGAA 840
GGCTGGACCG CTTGCTACTG GATAATCGTA GCCCTTCATG TTGCACCTTC TCCAGGTTCT 900
TAAGGGATTC TCCGTTTGGG TTCCATTTTG TACGAGTTTG GCAAATACGC TGCAGAAACG 960
AGCTGTGCTT GCAAGGACTT GATAGTTCCT AAGAATTAAA AACTCACTTG ATCAACTTAA 1020
TTCCCTTTTA TTTTTCCTCC CTCACTCCCC TTCTTTTTC AAGCTGTTTG CTTTGCAATA 1080
TGTTACTGGT AATGAGTTGC AGGTAATGCA ATCTTAACTT GTTTTCTTCT AAGTATTTGA 1140
GTTCAAAACT CCTGTATCTA AAGAAATACG GTTGGGGTCA TTAATAAAGA AAATCTTTCT 1200
ATCTTAAAAA 1210

```

## (2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1844 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: HW073
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 9..1223
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 598..1036
  - (D) OTHER INFORMATION: /label= SAC\_24456
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```

GTCGACCT GCC GGC CGA CAG GGC CGC GGG ATG AGG AAG CGG ACC GAG CCC 50
 Ala Gly Arg Gln Gly Arg Gly Met Arg Lys Arg Thr Glu Pro
 1 5 10

GTC ACC TTG GAG CAT GAG CGC TGC GCC GCC TCA GGC TCG TCT TCC TCC 98
Val Thr Leu Glu His Glu Arg Cys Ala Ala Ser Gly Ser Ser Ser Ser
 15 20 25 30

```

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| GGC TCG GCC GCC GCG GCG CTG GAC GCC GAC TGC AGC TTG AAG CAG AAC | 146 |
| Gly Ser Ala Ala Ala Ala Leu Asp Ala Asp Cys Ser Leu Lys Gln Asn |     |
| 35 40 45                                                        |     |
| CTG CGT CTG GCG GGC AAG GGG ACG GCA GAG CCG CAC AGC GCA TCC GAC | 194 |
| Leu Arg Leu Ala Gly Lys Gly Thr Ala Glu Pro His Ser Ala Ser Asp |     |
| 50 55 60                                                        |     |
| GCG GGC ATG AAG CGG GCT CTG GGC AGA CGG AAG AGC CTG TGG TTC CGA | 242 |
| Ala Gly Met Lys Arg Ala Leu Gly Arg Arg Lys Ser Leu Trp Phe Arg |     |
| 65 70 75                                                        |     |
| CTA AGG AAG ATA CTT CTC TGT GTT TTG GGG TTC TAC ATT GCC ATT CCA | 290 |
| Leu Arg Lys Ile Leu Leu Cys Val Leu Gly Phe Tyr Ile Ala Ile Pro |     |
| 80 85 90                                                        |     |
| TTT CTT GTC AAA CTG TGT CCT GGG ATA CAG GCC AAA CTG ATA TTC TTA | 338 |
| Phe Leu Val Lys Leu Cys Pro Gly Ile Gln Ala Lys Leu Ile Phe Leu |     |
| 95 100 105 110                                                  |     |
| AAT TTC GTG AGG GTT CCC TAT TTC ATT GAC TTA AAA AAG CCA CAG GAT | 386 |
| Asn Phe Val Arg Val Pro Tyr Phe Ile Asp Leu Lys Lys Pro Gln Asp |     |
| 115 120 125                                                     |     |
| CAA GGT TTG AAT CAC ACC TGC AAT TAC TAC CTC CAG CCC GAG GAT GAT | 434 |
| Gln Gly Leu Asn His Thr Cys Asn Tyr Tyr Leu Gln Pro Glu Asp Asp |     |
| 130 135 140                                                     |     |
| GTC ACT ATT GGA GTC TGG CAC ACC ATT CCC TCT GTC TGG TGG AAG AAT | 482 |
| Val Thr Ile Gly Val Trp His Thr Ile Pro Ser Val Trp Trp Lys Asn |     |
| 145 150 155                                                     |     |
| GCC CAA GGG AAG GAC CAG ATG TGG TAT GAG GAT GCT CTG GCT TCT AAC | 530 |
| Ala Gln Gly Lys Asp Gln Met Trp Tyr Glu Asp Ala Leu Ala Ser Asn |     |
| 160 165 170                                                     |     |
| CAC CCC ATC ATC CTG TAC CTG CAT GGG AAT GCA GGC ACC AGA GGA GGT | 578 |
| His Pro Ile Ile Leu Tyr Leu His Gly Asn Ala Gly Thr Arg Gly Gly |     |
| 175 180 185 190                                                 |     |
| GAC CAC CGT GTG GAG CTG TAC AAG GTG CTG AGT TCC CTT GGT TAC CAC | 626 |
| Asp His Arg Val Glu Leu Tyr Lys Val Leu Ser Ser Leu Gly Tyr His |     |
| 195 200 205                                                     |     |
| GTG GTC ACC TTC GAC TAC AGA GGT TGG GGT GAC TCA GTA GGA ACA CCA | 674 |
| Val Val Thr Phe Asp Tyr Arg Gly Trp Gly Asp Ser Val Gly Thr Pro |     |
| 210 215 220                                                     |     |
| TCA GAG CGA GGC ATG ACA TAT GAT GCA CTC CAT GTT TTT GAC TGG ATC | 722 |
| Ser Glu Arg Gly Met Thr Tyr Asp Ala Leu His Val Phe Asp Trp Ile |     |
| 225 230 235                                                     |     |
| AAA GCA AGA AGT GGT GAT AAT CCT GTG TAT ATC TGG GGC CAT TCG CTG | 770 |
| Lys Ala Arg Ser Gly Asp Asn Pro Val Tyr Ile Trp Gly His Ser Leu |     |
| 240 245 250                                                     |     |
| GGC ACT GGA GTG GCA ACA AAT CTG GTC CGG CGC CTT TGT GAG CGA GAG | 818 |
| Gly Thr Gly Val Ala Thr Asn Leu Val Arg Arg Leu Cys Glu Arg Glu |     |
| 255 260 265 270                                                 |     |
| ACG CCA CCA GAT GCC CTT ATA TTG GAG TCT CCG TTC ACA AAT ATT CGT | 866 |
| Thr Pro Pro Asp Ala Leu Ile Leu Glu Ser Pro Phe Thr Asn Ile Arg |     |

| 275                                                                                                                                               | 280 | 285 |      |
|---------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|------|
| GAA GAA GCA AAG AGT CAT CCA TTT TCA GTG ATA TAC AGA TAC TTC CCA<br>Glu Glu Ala Lys Ser His Pro Phe Ser Val Ile Tyr Arg Tyr Phe Pro<br>290 295 300 |     |     | 914  |
| GGC TTT GAC TGG TTC TTC CTC GAC CCC ATT ACA AGC AGT GGA ATT AAA<br>Gly Phe Asp Trp Phe Phe Leu Asp Pro Ile Thr Ser Ser Gly Ile Lys<br>305 310 315 |     |     | 962  |
| TTT GCA AAT GAC GAA AAC ATG AAG CAC ATC TCC TGT CCC CTG CTC ATC<br>Phe Ala Asn Asp Glu Asn Met Lys His Ile Ser Cys Pro Leu Leu Ile<br>320 325 330 |     |     | 1010 |
| TTG CAC GCT GAG GAT GAC CCA GTT GTA CCC TTT CAT CTC GGC AGG AAG<br>Leu His Ala Glu Asp Pro Val Val Pro Phe His Leu Gly Arg Lys<br>335 340 345 350 |     |     | 1058 |
| CTA TAC AAT ATT GCT GCG CCA TCC CGA AGT TTC CGA GAC TTC AAA GTC<br>Leu Tyr Asn Ile Ala Ala Pro Ser Arg Ser Phe Arg Asp Phe Lys Val<br>355 360 365 |     |     | 1106 |
| CAG TTC ATC CCC TTT CAC TCA GAC CTT GGC TAC AGA CAT AAG TAC ATC<br>Gln Phe Ile Pro Phe His Ser Asp Leu Gly Tyr Arg His Lys Tyr Ile<br>370 375 380 |     |     | 1154 |
| TAC AAG AGC CCA GAG CTT CCA CGG ATA CTG AGG GAA TTC CTA GGG AAG<br>Tyr Lys Ser Pro Glu Leu Pro Arg Ile Leu Arg Glu Phe Leu Gly Lys<br>385 390 395 |     |     | 1202 |
| TCG GAA CCA GAG CGC CAG CAC TGAGCCTGGC CCGTGAAGGA GCATGGAGAC<br>Ser Glu Pro Glu Arg Gln His<br>400 405                                            |     |     | 1253 |
| CCACCTTCCT TCCCTTCTCC CTGAACAGCA GTCTGGCACC CAGAAGCTCA GAGTGCCACC                                                                                 |     |     | 1313 |
| ACCTGTGGTG CTCAGGAGCC CAGCCTAGAA AGAGGACTCC GACACAGCGG GCAGAGGCTC                                                                                 |     |     | 1373 |
| CACAGACGGA TCTATGAGGA AAATACGGTG GCAGGCAGGC AGGCAGGCGA CCCCCTGACC                                                                                 |     |     | 1433 |
| CTCTGGTGGC CGCTGTATCT GAGCCCTTTT GGGAAGGCTT ATAGACAACA GGTGGAGCCC                                                                                 |     |     | 1493 |
| ATACGCTGGG CATAGGGAGC CTGGGAAGGG CTCAGGAGCT CAGGACCACT CCAGGCTCTC                                                                                 |     |     | 1553 |
| TAGCACCACC GCTTAAAATA CAGGAAAAAG GTTCTTTCTG CCCTTCCTGG CGTACACAGA                                                                                 |     |     | 1613 |
| ACAGATTCCA AGTGGTTCAA TTTGTCCCTT ACAGCTCATG TACCTGCTTG CCTTCCTCAG                                                                                 |     |     | 1673 |
| CTGTCCCTGC CTCTCCTGGC ATCTGTACAC CCACAGTGAG GGGCACCTGG ACTTGCACTT                                                                                 |     |     | 1733 |
| CCATTCTGCC CACCTGTCTG TCACCTAACC TGGCCGTAGA CTGAGCATTT ATTTAAGAAT                                                                                 |     |     | 1793 |
| AAAATCTCGG TGGTGGTCTA TTTGTTTTTT TCTACAAAAA AAAAAGTCGA C                                                                                          |     |     | 1844 |

## (2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 405 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Ala Gly Arg Gln Gly Arg Gly Met Arg Lys Arg Thr Glu Pro Val Thr  
 1 5 10 15  
 Leu Glu His Glu Arg Cys Ala Ala Ser Gly Ser Ser Ser Ser Gly Ser  
 20 25 30  
 Ala Ala Ala Ala Leu Asp Ala Asp Cys Ser Leu Lys Gln Asn Leu Arg  
 35 40 45  
 Leu Ala Gly Lys Gly Thr Ala Glu Pro His Ser Ala Ser Asp Ala Gly  
 50 55 60  
 Met Lys Arg Ala Leu Gly Arg Arg Lys Ser Leu Trp Phe Arg Leu Arg  
 65 70 75 80  
 Lys Ile Leu Leu Cys Val Leu Gly Phe Tyr Ile Ala Ile Pro Phe Leu  
 85 90 95  
 Val Lys Leu Cys Pro Gly Ile Gln Ala Lys Leu Ile Phe Leu Asn Phe  
 100 105 110  
 Val Arg Val Pro Tyr Phe Ile Asp Leu Lys Lys Pro Gln Asp Gln Gly  
 115 120 125  
 Leu Asn His Thr Cys Asn Tyr Tyr Leu Gln Pro Glu Asp Asp Val Thr  
 130 135 140  
 Ile Gly Val Trp His Thr Ile Pro Ser Val Trp Trp Lys Asn Ala Gln  
 145 150 155 160  
 Gly Lys Asp Gln Met Trp Tyr Glu Asp Ala Leu Ala Ser Asn His Pro  
 165 170 175  
 Ile Ile Leu Tyr Leu His Gly Asn Ala Gly Thr Arg Gly Gly Asp His  
 180 185 190  
 Arg Val Glu Leu Tyr Lys Val Leu Ser Ser Leu Gly Tyr His Val Val  
 195 200 205  
 Thr Phe Asp Tyr Arg Gly Trp Gly Asp Ser Val Gly Thr Pro Ser Glu  
 210 215 220  
 Arg Gly Met Thr Tyr Asp Ala Leu His Val Phe Asp Trp Ile Lys Ala  
 225 230 235 240  
 Arg Ser Gly Asp Asn Pro Val Tyr Ile Trp Gly His Ser Leu Gly Thr  
 245 250 255  
 Gly Val Ala Thr Asn Leu Val Arg Arg Leu Cys Glu Arg Glu Thr Pro  
 260 265 270  
 Pro Asp Ala Leu Ile Leu Glu Ser Pro Phe Thr Asn Ile Arg Glu Glu  
 275 280 285  
 Ala Lys Ser His Pro Phe Ser Val Ile Tyr Arg Tyr Phe Pro Gly Phe  
 290 295 300  
 Asp Trp Phe Phe Leu Asp Pro Ile Thr Ser Ser Gly Ile Lys Phe Ala  
 305 310 315 320

```

Asn Asp Glu Asn Met Lys His Ile Ser Cys Pro Leu Leu Ile Leu His
 325 330 335
Ala Glu Asp Asp Pro Val Val Pro Phe His Leu Gly Arg Lys Leu Tyr
 340 345 350
Asn Ile Ala Ala Pro Ser Arg Ser Phe Arg Asp Phe Lys Val Gln Phe
 355 360 365
Ile Pro Phe His Ser Asp Leu Gly Tyr Arg His Lys Tyr Ile Tyr Lys
 370 375 380
Ser Pro Glu Leu Pro Arg Ile Leu Arg Glu Phe Leu Gly Lys Ser Glu
 385 390 395 400
Pro Glu Arg Gln His
 405

```

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 855 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (vii) IMMEDIATE SOURCE:

- (B) CLONE: HW074

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..300

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: complement (64..365)
- (D) OTHER INFORMATION: /label= SAC\_24464

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

GTCGAC AGC CCT CGA GGG AGC AGA CGC CGC GGG CCA CTG GCT TCC TCT 48
 Ser Pro Arg Gly Ser Arg Arg Arg Gly Pro Leu Ala Ser Ser
 1 5 10

ACT CAG GAA CCA CGG ATG TCA CCG CCC AGT CAG CTG TGT CTC CTC ACC 96
Thr Gln Glu Pro Arg Met Ser Pro Pro Ser Gln Leu Cys Leu Leu Thr
 15 20 25 30

ATT GTC GCC CTG ATT CTG CCT AGT GAA GGG CAG ACA CCA GAA AAA CCC 144
Ile Val Ala Leu Ile Leu Pro Ser Glu Gly Gln Thr Pro Glu Lys Pro
 35 40 45

AGA TCC AGT TTT ACA GCG CAC CAG AGT TCT GTG ACT ACT CAT GTC CCA 192
Arg Ser Ser Phe Thr Ala His Gln Ser Ser Val Thr Thr His Val Pro
 50 55 60

GTT CCA GAT CAA ACT AGC CCA GGA GTC CAG ACC ACT CCT CCC ATC TGG 240

```

Val Pro Asp Gln Thr Ser Pro Gly Val Gln Thr Thr Pro Pro Ile Trp  
65 70 75 288

ACC AGT GAA GCT GCG AAG CCA CAG GAA GCC AGA CAG CAG CCA AAA CCA  
Thr Ser Glu Ala Ala Lys Pro Gln Glu Ala Arg Gln Gln Pro Lys Pro  
80 85 90

AGA CCC AGC AAC TGACCGAAAT GGCCACTGCG AATCCAGTGA CAGATCCAGG 340  
Arg Pro Ser Asn  
95

GCCACTTACA AGCAGCGAGA AAGGTACCCC GGCACCTCTCC AGGATCAAAT CTCCCAGCCC 400

ACCCAAAGGT TACATGCCTC CATCCTACAT TGAGAATCCA CTGGATCCCA ATGAGAACAG 460

CCCCTTCTAC TACGACAATA CCACCCTCCG GAAACGGGGG CTGCTGGTGG CGGCAGTGCT 520

GTTCATTACT GGAATTATCA TCCTCACTAG TGGGAAGTGT AGACAGTTCT CTCAGTTATG 580

CCTGAATCGC CACAGGTGAG TGGGAGCCAG CACCCTGATG GGCACCCCAA CTGGAGCCGC 640

CATACCATAC CAGTTCACCA CCCCTGCCTC CCTCCCTCTG CTCCAAGAGC CAACAGAGTG 700

GTCAACATAA ATGGATCCTC AAAGGAAGAG GCCACCGGAG GGAGCCAGGC CTAAGGCTAA 760

ATGGTCTTCC CACCCTGAGG AGAGAGGTCT CCCAGGCAC TGCTGTGATC CTGCCTATCC 820

TGTTTCAGATA AATCCACATG GTCTCTCTTC AAAAA 855

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ser Pro Arg Gly Ser Arg Arg Arg Gly Pro Leu Ala Ser Ser Thr Gln  
1 5 10 15

Glu Pro Arg Met Ser Pro Pro Ser Gln Leu Cys Leu Leu Thr Ile Val  
20 25 30

Ala Leu Ile Leu Pro Ser Glu Gly Gln Thr Pro Glu Lys Pro Arg Ser  
35 40 45

Ser Phe Thr Ala His Gln Ser Ser Val Thr Thr His Val Pro Val Pro  
50 55 60

Asp Gln Thr Ser Pro Gly Val Gln Thr Thr Pro Pro Ile Trp Thr Ser  
65 70 75 80

Glu Ala Ala Lys Pro Gln Glu Ala Arg Gln Gln Pro Lys Pro Arg Pro  
85 90 95

Ser Asn

## (2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4315 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: HW075
- (ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: complement (3785..4014)  
 (D) OTHER INFORMATION: /label= SAC\_24466

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| GTCGACATGG CGAAGTACTC TAGCCTGGAA GCCAAGCTCT GCCAGGTTGA AAGTAAATAC | 60   |
| TTGATACTGC TCCAAGAAAT GAAGACACCA GTTTGCTCAG AAGAACAGGG CCCTGCCAGG | 120  |
| GATGTCATAG CCCAGTTGTT GGAGGACGCT CTGCAGGTTG AGAGCCAAGA GCAGCCAGAG | 180  |
| CAAGCGTTTG TCAAGCCTCA TCTGGTCAGT GAGTTCGATA TCTACGGGTT TAGGACTGTC | 240  |
| CCTGACGATG ATGAGGAAGA GAAATTGGTC GCCAAGGTCC GAGCATTGGA CCTGAAGACT | 300  |
| CTGTACCTCA CAGAAAACCA GGAAGTTTCC ACTGGGGTCA AGTGGGAAAA CTATTTTGCA | 360  |
| AGCACAATGA ACAGGGAGAT GGTGTGCTCT CCTGAGCTGA AAAACCTGAT CCGAGCAGGC | 420  |
| ATTCCCCATG AGCACCGCTC CAAGGTGTGG AAGTGGTGTG TTGACCGTCA CACCAGGAAG | 480  |
| TTCAAGGACA GCATGGAGCC AGGCTACTTC CAGGCCTTAC TCCAGAAGGC TCTAGAGAAA | 540  |
| CAGAACCCGG CCTCCAAGCA GATTGAGCTG GACCTGCTTC GGACTCTGCC CAATAACAAA | 600  |
| CATTACTCCA GCCCCACGTC AGAGGGCATA CAGAAGCTTC GCAATGTCCT GCTTGCCTTC | 660  |
| TCATGGAGGA ATCCGGATAT TGGCTACTGC CAAGGCCTAA ACAGGTTGGT GGCAGTGGCG | 720  |
| CTCCTTTACC TGAACAAGA GGATGCTTTC TGGTGTCTCG TTACCATTGT GGAAGTCTTC  | 780  |
| ATGCCTCGAG ACTATTACAC AAAGACTCTA TTAGGATCCC AGGTGGACCA GCGGGTGTTC | 840  |
| AGAGACCTCC TGAGTGAGAA GCTGCCTCGA CTGCACACCC ATTTTGAGCA GTACAAAGTG | 900  |
| GACTACACCC TCATCACCTT CAACTGGTTT CTGGTGGTAT TCGTGGACAG CGTTGTCAGC | 960  |
| GACATCCTCT TTAAGATATG GGACTCTTTC CTTTATGAGG GACCAAAGGT TATTTTCCGT | 1020 |
| TTTGCCCTGG CACTTTTTAA ATACAAGGAA GAGGAGATCC TGAAGCTGCA GGATTCGATG | 1080 |
| TCCATTTTCA AGTATCTCCG ATACTTCACT CGCACTATCC TTGATGCCAG GAAGCTGACC | 1140 |
| AGCATCTCCT TTGGGGATCT GAACCCCTTC CCCCTGCGCC AGATCCGGAA CCGGAGAGCC | 1200 |

|            |            |            |             |             |             |      |
|------------|------------|------------|-------------|-------------|-------------|------|
| TACCACTTGG | AGAAGGTCCG | GCTGGAGCTG | ACAGAGCTGG  | AGGCCATTCTG | AGAGGACTTC  | 1260 |
| CTGCGTGAGC | GGGACACTAG | CCCTGACAAA | GGCGAGCTGG  | TTAGCGATGA  | GGAGGAAGAC  | 1320 |
| ACTTGAATGA | ATCCCCACCC | CAGGATGCTG | CCTTCCTTCT  | TGCCTTCCTT  | CATAACCAAA  | 1380 |
| AGTAGCAAAG | GCGCATCTGC | ACATCAGCTG | TCAGAGTGAA  | ACATCTACAG  | CCTCTGGGCA  | 1440 |
| CCTGCGGGGC | AGATGTCCAA | AGCTAAGCTG | CACTTTCTCG  | TCTGCCATGA  | GGGCAGGGGT  | 1500 |
| CTGATGGCTT | TACAGCCATT | TCCATGCCGT | GGCATTCTAGT | CATATGCGTC  | ATATGCTTGC  | 1560 |
| TGCCTGATGG | GTGAGTCACC | AGGCGACTGT | TTCCAAGGGC  | CTGTTTACAT  | CATCTGCCAG  | 1620 |
| TTGTATGTTT | CACCTACAGA | AACTGTTTGA | CATTTCCCTG  | TGCGCTTCT   | TTTTATCCAA  | 1680 |
| GGGCAACTCT | GTGGAGGAGT | GCACATGGAG | CTGCAGCGTG  | GCTGCATCCA  | GGGGTAAAAAG | 1740 |
| GTCACCATAA | GAAGAGGGAC | CTCTTTAAAA | AAAAGCGAGC  | ACAGAACTGG  | CCTCCCTAGA  | 1800 |
| GAGCGTGGA  | GCCCTCTGCT | GGTGGCTTCG | CACTGCCAGC  | CACTATCCCT  | TCTGGACTAA  | 1860 |
| CCTTTGCCCT | CCTATACAGC | CTTTTCAGAT | TGTAGCACTC  | ACGCTGCTCT  | GCAGCCAGCC  | 1920 |
| CCCACTTCT  | CATTGCCAGC | TATTCTGCCA | GATGTCTGTC  | CCAGCTTACA  | GTGGGGCTAG  | 1980 |
| CGCATCTGGG | AGGTGACTTA | TAGACAACAT | TCTCCAAC TG | TGGCTAGATT  | GGCGTTCCAA  | 2040 |
| AGGAACCTTA | CAGTAACCCA | CCCCTGCATA | AAGGAACACA  | GGAAACTCCT  | ATCTGTGGCT  | 2100 |
| TGTGGGCTCC | TGGATGGCAG | TGGCCAGGGC | TCTAGAATCT  | CTTCTGCCCA  | ACAGCTGGGT  | 2160 |
| GGGGAGTAGA | GCTGACTGCC | AGCTTCCTAC | ATCTGGAAGC  | ACCTTTGCTT  | GGGAACAAGA  | 2220 |
| GTAATGAGTT | CTCCTAGTCT | CTGTGTTGCC | TGGATCATCC  | TTGTCCTTAA  | CAGGGATCTG  | 2280 |
| AGGACACTGT | GGCCTCTGGT | ATAGCAGACT | CTGGGGACTT  | GGAACACTTC  | CTTCTTGAAG  | 2340 |
| CCCAGAGAGG | GTCTGAACAA | AAAAGGTTAT | TTTTGCTCAG  | TCCCAGAGCA  | TCCCTAATGG  | 2400 |
| TGGCTGTTAT | GAGAAAACAT | CTTCTTACAC | AGTATTATGG  | GAACACAAGG  | GAAACAGCCT  | 2460 |
| CAAGTGGACT | ACTTTACACT | ACCTAGGGAA | AAGAAATTAG  | AAACAATCCT  | TAGTGTA AAC | 2520 |
| ACACTCAGAC | TGAGGAGTGG | AGCAAGACAG | TTTCGAGAAA  | CGCTTTTTCC  | ATGACCCGTT  | 2580 |
| TTCTGTGTTT | TGCTGTCTGC | TTTCTAGCAC | TTGAATGGCT  | GAGTCCATTT  | TCAGCATCTA  | 2640 |
| AATTTGCTTC | ACTTCTCTAA | AGTTGCTTCA | TATATTACCA  | TGTAAAAGGA  | GCTGGTCTCT  | 2700 |
| ATATTTAGCC | AATAGCCCGT | CTCTTTTCAG | GTATCAGAAA  | TGTCATCCCT  | GTGTCTTTGA  | 2760 |
| GATGATGGTT | TGAGGCCCGG | CTTCTTGAAG | AAGCTGTCTG  | GAGCTGGACA  | GTGATCTATC  | 2820 |
| TCACCACTGT | TCCTAGGCCT | CCCTGAGACC | AAATGCTGGA  | AGATGCCCCA  | CCCCCTGTAA  | 2880 |
| GATGCCGGCT | GTCAGCCTTG | GGGACAGCTG | TTAGGAGGTT  | AGAGTTGGAG  | CCCCATGGCT  | 2940 |
| TAGCTCCAGC | CGCTCTGATT | TCGGTTGTCA | TGTCAATTTT  | CTACCAGAAG  | ATCCAGTCCA  | 3000 |
| AATAAGTATT | TGGTGTGGAT | GCTCTCAGTG | GAGCATTTGG  | TGTGGATGCT  | CTCAGTGGTG  | 3060 |
| GGTTGCTTTC | GCCCTGGCAC | CAGTGGAGGC | ATCTTTAAGT  | ACTTGGTGAT  | GCTGAGGACA  | 3120 |

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GGACCATGTT CCTGGCATGC GGGGCCCTGG GTTCCATCCC AGTGATGAAA AAAAATCTTC 3180
AGTATGTGGG GATTGTGGGG AGGCGCTGTT CTGCCATCCC CTGAGAGACA GCATTAGTTT 3240
CTCAGGCAGT TAGTATCAGT GCCCAGGTAA AAGTCTCAAG AGGTCCCAA GGGACTCTCC 3300
TCCCTGGAAT AAATGACTCG ATGTCTGCAG AGCGGAGAAG GGACGGTTGC CCTCTTTCCA 3360
GTTTGGGGAC AGAATAACAG AGATTTCATCC CAGAGGCACA GCCCCAGTGG TTGAGCCATC 3420
GTCTCTCATG CCCTCGTCAC TGAGATTGTC TTTACCCTCC AGTACTCCTG AGACTCCAGA 3480
CTTCTACCAG ACACCATGGC AGGTACCCCT AAGGTCAGTG GCTGCCTCAG GCTGCTTTTC 3540
ATCTAAACCT TTACCCAGCA TGCAACCCAT GGCTCCTGCC TGGTGAGCCT TGTGGGCTGA 3600
GAAACCCAAA GCACAGCCTC CAGCGCGTGG GTCCAAATGC GTGTGCCACA GTAGGGGAGC 3660
ACCTTGCCCT CAGCACCCCA TATGGTGGGA CTTGCCAGTA TTTCAACTGT TGATACTTTT 3720
ATATTTTCAC TACATTTTAT ATTTTATAG ACTATTTTAT ATTAAGGTTT TTTCTAGATT 3780
CTGTACAAC TTTATATAAC AAGTTCATT TTGTGTGCAC ATCTCCCCTG TATGTATTTA 3840
TAGCAACCCA AGCCTCTCAA ATTCCAGGTC CCTCTGTGC CACCTTTTCC CTTAGCCTT 3900
GACTGTCACT CTCTTCTGCT CACCGAGGTA GCCTCGGGG CTACTTCTAG CCACCATGAC 3960
AGCCAGACAG CAGGAACCTG TGTTTGTCAG CTGTGGTCTG TTGATACAGG AAGTACTCTG 4020
GGCAGTAACC CAGTAGCTAT GTTACTGCAC AAGCCCTTCT CGCTTAGTGC AGTGATGTCC 4080
TGGTGCAGCC ACCTGTGGGC GGGTGGCTGG ACCCATCACG AAAGTCCTTG AAGACAGAGG 4140
CTAGATGAAA GCCCAGTGTC TGAGGTCCTT CTGTGGGCAA CTGGAGGACT TGAGGGCACA 4200
CTGCCAAGTG ACTGTCCTTT TATATCCTAG CAGCTTCTGT GCTCACCTT GAGTTAAATG 4260
TTAGACTTTT AAAGGAAGAA ATAACTAAT TTGTATTACA TTCTGCCTCG AAAAA 4315

```

## (2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1668 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: HW076
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: complement (42..281)
  - (D) OTHER INFORMATION: /label= SAC\_24409

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

|                                                                   |      |
|-------------------------------------------------------------------|------|
| GTCGACTTTT GCCTTTAAAA TTCTGTTTAC TTAGCATATG TACACGTAAA AGAGAAATCA | 60   |
| CCCTTAGATC CCACCCAGCA GAAAACATGC ACAAACCCAA GGTATATGTG AAAGGGAGGG | 120  |
| CCCCAGCCCC AAGTTAGCAG TTGGGATGGT GCAATCCTGT GAGTCACAAG CCCATGGCAA | 180  |
| GAGGGCTGGA CTAAAGTTTC AACACAGCCA GAACCCCTGC TGCTGGCCCT AAAATAAGCG | 240  |
| TGCACCATAG CCAAAGGTCT GTTTGATGCC CTCAAAGTAG TACCGCTGCC AGCCTTGCCG | 300  |
| TGTCCGCTCT TCCTCGGGAG CAGGGATGCC GCGGCCCTCC ATGCACAGCT CTGTCTCTCC | 360  |
| ATTCTTATCA ATGAAGGTCA AGGTGATGGT CGCGAAGTGC CCCTCTGGCC ATGACTTAAA | 420  |
| CCTCCACTTC ATAGCAATAT GTTCTCAGG AACCAAGTCA GTAAACTCCC CAGTGACGTT  | 480  |
| ACCATCGACC ATGTGAAACT TCCCTCCTCT GTCTGCTTCC AAGGCCGAG GAGCATGGGT  | 540  |
| AAAGGCCTGG ACCAGCTCCT GCGTGGTGAA CACTCTGTAG AGCTCCTCTG GAGAGGTCAG | 600  |
| GAAGGTTTCT TTGAGGGTGA TCTTACAAGT GGGTATTTTG ACACCAACAG GTTTGGCCTG | 660  |
| GCTTTTGTGA GGAGCACACT TAGCCTTGCA CACTTCCGTT TTAGTGCTG GTTGGCCAC   | 720  |
| TGGGTCTACT GATTCCTCAT TCACTGTGGG CAAGATCATG CCCTGAGTAA ACTCTGTCTT | 780  |
| GAGGGTGCTG ATGTAAATTC CCACTGCTTC TCTGAGAAGT TTCACCCCGT CTCCTTCAT  | 840  |
| TAAGGCCACG AGACTTGTGT CAGGCTCATC TTTGGCAAGG CTGCTTCTTA GAGCCCTTGT | 900  |
| TATGGCAGCG CTCCATCTAG GAAACAGCAG TCAGTCTCTC CTGCTCACTG TTCTCCCTCT | 960  |
| CTGTGCTCAA GTCTGTCACT GCTCGCTGGC CTCTGGCTCT TCCCTTTGGG GAGGGAGCGG | 1020 |
| CTGTTCTGCC TGCTTCACCG AGTCTTCACA AGCTGAGGGG ATGAGGCCAG GTTAGTACCA | 1080 |
| GGGACCAGCA ACCTTTCAGG GCTCCTTGGG GGTCTCAGGT CCACACACAG TGAGCATCCC | 1140 |
| TTGCCAGGTG CCCCATGTAT CTGTCACTGC TGAGACGCCA AACACACAAC CTGTTCCAG  | 1200 |
| CTGTGCTGCG GGGCCACTGT GACCGAGGAG AGTGTGGGGT TGCCAGGGAG AGCGCTGTCC | 1260 |
| CTCTGACAGC CTGACCAGAT GATGTAGCTT TGAAAGCCGG CAGCATGTGA GTAGCAAGAT | 1320 |
| GTGACCTTGA GCTAGCTGAG CAGAACACAG GTGGATGGGC AGAGGCCCCC ATCCTGGCGA | 1380 |
| GCTGAGCCTG GCTGTGTCCT GTCAGGACGC CCTACTCTGT GACCCTACCC TGTGATCTGT | 1440 |
| GAAGTGGTGC AGTCGGAAGA CGAGGCTGGA GTCCTTTACA AGTTTCTACA CTAGATTGTA | 1500 |
| GCCAGGTTTT CTCCCAGGCC TTAGGCTTTG GTTTACTTTT AATTTTAATT TCACTGTTAC | 1560 |
| CCTTGACTAT TGTCTTTTTT GTTGCAGTGT TGGAGAGGCA GGAGGTATTT GTGCCTCATC | 1620 |
| TATTAAGTGA AAAAAATTAA ATAAATGTAA CAATAAACGT CCTAAAAA              | 1668 |

## (2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1019 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: HW078

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: complement (211..743)  
(D) OTHER INFORMATION: /label= SAC\_24345

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| GTCGACGCCA GCGTGAGCGC CCTGCAGCGC CTGGTGAGAGC AGCTGAAGCT GGAGGCCGGC | 60   |
| GTGGAGAGGA TCAAGGTCTC TCAGGCAGCT GCAGAGCTTC AGCAGTACTG CATACAGAAT  | 120  |
| GCATGCAAGG ACGCCCTGCT GCTTGGTGTTC CCGGCTGGAA GCAACCCCTT CCGGGAGCCC | 180  |
| AGGTCCTGTG CTTTACTTTG AAGACTGGGA AGAAGCTCTC TGAGGAACCT GTGTGTGCAT  | 240  |
| GGTGATGGAT GACTACCGCC AAGTCCCAAG AAAACAGATT TCAAGAGCCA AATCATTTTC  | 300  |
| TCTGTGGCCT GGTCCCTAGGT CAAAATTCTA CAGAAATCAA TGTTTTGTCT TATTTTTTAA | 360  |
| CCTCATTACC AAACCTACTG GGTGCATCTC TCAGTCAAGC CTGTGCGGCC CTGCCTGGGA  | 420  |
| TGGAGGCATG TTTTGTFTAC TGGGTATTTG CATTTCTGGA TGGAAATGTT GTATTTCCGA  | 480  |
| AAACTGAGTA TTTGTAATTT TCCTAACATT TTTATACTGT AATAAAAAAT TTTCATAAAA  | 540  |
| ATTTACAGTT ACTAAATTAG ACAAAGTATA AATTGGGGAA TGATTGATAT GCTGGTTTCG  | 600  |
| TAAAGGAGGC CTTTCCAGTC CCAGTGAGCA AACGGTCTGA CCTGGACGGG AAGCTGGGGA  | 660  |
| GCCGCTCCTT AGCACACGGA GCATGGATGT GTTGTTAGGT GGCCCTCCCG TGTGAAGCCA  | 720  |
| TTAGAACTTT CTTTAGTTCC TGTACTCTAC AACTTATAAT TGTGTCTGAT GCTTTGAAAA  | 780  |
| GTGTGCTCAT GCCTTTAAAA ATGTTTAAAT GTGATCTACA CTTAGAACGT TGCAATTGGT  | 840  |
| TAAAAACAAA ATATGAAGAT ATTATAACCT AAAAGAATTC ATGTCACACA TATTTTATTG  | 900  |
| GGGGTGATGT GCCTTTGATT TAATTGGGGA CACTTTTAGA AGGAAAGTTT GTGTTTGTGA  | 960  |
| TTATCTTTGA AGAGCTTGGA AATAAAATTT TTGCCTAATT CATCATTTTC CATGAAAAA   | 1019 |

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 961 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: HW080
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: 629..919
  - (D) OTHER INFORMATION: /label= SAC\_24033

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

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GTCGACGCTG GGCAAAAGAA GGTTCACCA GAGCCTGTGG GTTGTCTCTT AGGCTAGAGG 60
CCCCAAGATT TGGAACCTGG TGGAATCAGT AGGAGGGACA TTGAAGCTCA CAGATATATC 120
ACACGTTGGT CAGTTGCTTC TGCAACTGGT CCGTTAGGTG CTGTGGGACG AGCCCTTTCC 180
TACCTTCTTC AGCTTCTACA TCCACTGTCT GCCTGTGTCT CAGTTTACAT CTTCTTTTGG 240
AATATGGAAT CTCAAATAGC CCAGGCTAGC TTCAAATTTG TTAAGTAGTT GAGGACAACC 300
TCAATCTTTC TATTCGCTGC CTCCACCTCT CTCAGTTTAC CTTTTTTTTT TTTCTCCTTA 360
GGATTAAAGTC CCGTACAGGC CCAGAGTGGT AAGCCATAAC ACCCCTGGTC TTTCTCTCTT 420
CCTCTCAAGA TTTCTCAGG CTACCCCTTT TCCTTCTAGC TCTCTCTCTC TGCTAACGCC 480
GAGCCCTGAT TGTTAACTG TGTCCTCCCTC TTCATCCTTC TGAGACAATT ACCCAGGATG 540
CGAATGTTCC TCTGTGAGCC CGGGTGTACT GGCTGGGATT GTGCTGGGCG ACTTGGTGCT 600
GACTCTGCTC ATCGCCCTGG CGGTGTACTC TCTGGGCCGC CTGGTCTCTC GAGGCCGAGG 660
GACTGCAGAC GGGACCCGGA AACAGCACAT GGCTGAGACT GAGTCACCTT ATCAGGAGCT 720
TCAGGGTCAG AGGCCAGAAG TATACAGTGA CCTCAACACA CAGAGGCAGT ATTACAGATG 780
AACCCACCTT ATGCCCACCA ACAACCTGAT GCCCGGATCC ACTCATTCCA GACGCTTACT 840
CAACAAACCC TCCCTGGGAT CAGGACTCCC GCTGGAATAA ATATCCACAG AGTGCCCTCT 900
GGGAGATATC TGACCTTGTA CCGTTTCTGT CCCCAAATAA AAGACGAAGC AAAAACAATA 960
A 961

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## (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1890 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: HW082

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 150..569

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1381..1848  
(D) OTHER INFORMATION: /label= SAC\_24469

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GTCGACCGCG GCCGCGTCGA CGGACTTGCG GTTCCTTCAG CATTCTGCCC GCGCACTGAG | 60  |
| TGGCTGT TTC CTGGAGCTAC TGTGTTCTT CGGGAGTGCA GCAGATCCCG TTCAGAACCT | 120 |
| ATTACCAAGA GCCCCGAGCA GGACCCACC ATG CAG TGC TTC AAA TTC ATT AAG   | 173 |
| Met Gln Cys Phe Lys Phe Ile Lys                                   |     |
| 1 5                                                               |     |
| GTC ATG ATG ATC CTC TTC AAT CTA CTC ATC TTT CTC TGT GGT GCA GCC   | 221 |
| Val Met Met Ile Leu Phe Asn Leu Leu Ile Phe Leu Cys Gly Ala Ala   |     |
| 10 15 20                                                          |     |
| CTG TTG GCT GTG GGA ATC TGG GTG TCC GTC GAC GGG ACA TCT TTC CTG   | 269 |
| Leu Leu Ala Val Gly Ile Trp Val Ser Val Asp Gly Thr Ser Phe Leu   |     |
| 25 30 35 40                                                       |     |
| AAG GCC TTC GGA TCA CTA TCA TCG AGT GCC ATG CAG TTT GTC AAC GTG   | 317 |
| Lys Ala Phe Gly Ser Leu Ser Ser Ser Ala Met Gln Phe Val Asn Val   |     |
| 45 50 55                                                          |     |
| GGC TAC TTC CTC ATC GCC GCT GGT GCT GTA CTC TTT ATT CTT GGT TTC   | 365 |
| Gly Tyr Phe Leu Ile Ala Ala Gly Ala Val Leu Phe Ile Leu Gly Phe   |     |
| 60 65 70                                                          |     |
| CTG GGC TGC TAT GGT GCT CAC TCC GAG AAC AAG TGT GTG CTC ATG ATG   | 413 |
| Leu Gly Cys Tyr Gly Ala His Ser Glu Asn Lys Cys Val Leu Met Met   |     |
| 75 80 85                                                          |     |
| GTG TGT TGG ACC CAG CTC CCC AGG CCC ACA ACC AAG GGT TCC CCC TTC   | 461 |
| Val Cys Trp Thr Gln Leu Pro Arg Pro Thr Thr Lys Gly Ser Pro Phe   |     |
| 90 95 100                                                         |     |
| ATC CCT GAC ACC AGC CTC TGG GAT CCC AAA ACC CTA CTC TGG ATT CTG   | 509 |
| Ile Pro Asp Thr Ser Leu Trp Asp Pro Lys Thr Leu Leu Trp Ile Leu   |     |
| 105 110 115 120                                                   |     |
| GAA GCC TCG CTG TGG GGA CCC CCT GCC TCT TAT GGG AGT GTG CAG GAA   | 557 |
| Glu Ala Ser Leu Trp Gly Pro Pro Ala Ser Tyr Gly Ser Val Gln Glu   |     |
| 125 130 135                                                       |     |
| GGT GTG TAT CCC TAAAACGTGT TTCCTTTCTC CACTCAGTTC TTTTCCATTC       | 609 |
| Gly Val Tyr Pro                                                   |     |
| 140                                                               |     |
| TCCTCATCAT CTTCATTGCG GAGATTGCAG GGGCCGTGGT TGCTTTGGTG TACACCACAA | 669 |
| TGGTGAGGCA CGGGATGGGG CATGGGAGGA AACTGGAGC AAAGCTCTGA GAGTTGGTGG  | 729 |

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TGGCCTGTGA ATGGCTACTT CCCCTACCAG TCTATTAATA CTGGCCTGAC CCGTCCAGGC 789
TGAACAATTC CTGACATTTC TGGTGGTGCC TGCTATCGAA AAGGACTATG GTTACCAGAC 849
TGAATTCACC CAAGTGTGGA ACTCTACGAT GGAGGGGGTA AGGTGGGCCG GGAGGATTTG 909
GGAATGGAGA GGAGAAAAAA ATCAAGGCAC CATCAGTTAC CAACCCCAT TTTGTCTGCAG 969
CTGCATTGCT GTGGCTTCAA CAATTACACA GATTTTAACT CCTCACGTTT CGTCAAAGAG 1029
AACAAAGTCT TTCCTCCGTT CTGTTGCGCC AACAACTACT ACAGTCATAC AGTTGAACCA 1089
TGCACCGAGG ACAAGGCCAA AAGTATGAAC GTACAGGTAT GTGCTGGTGT GGAATTAGCT 1149
TTTTCGTTTG TGATCCGTTT TCTCTGTGTA GCTGTGGATG TCCTGGAACG CGATATGTAG 1209
ACCAGGCTGG GCTTGAACAG AGATCGACCT GCCTCTGCCT CCTGAGTGCT GGGGTAAAG 1269
GCCACCATCA CCACCCAGCG CCAGTGTAAT TGCTTTAATG GCTTTACAGT AAGGAGTAAA 1329
GGGGTTGGAG GTAGGGCACT GCCAGCTATA AATACTTTCT TCTCTCTCCC AAGGGTTGTT 1389
TCAAACAGAT TCTGCAGAAA ATCAGAACCA ATGCAGTTAC CGTGGGTGGT GTGGCAGTTG 1449
GAGTTGCGGC CCTAGAGCTG GCTGCCATGG TGGTATCCAT GTATCTATAC TGCAATCTGA 1509
AGTAAGACTG CTTCTTCCTC CTGACTTGTC GTCACATGGA AACCAGGAAG AGGCACTTGG 1569
CACAGCTAAG CAGCAGCAAT GGGTGGAGAT GAAACGTCAT TTGGGCTGGA GTGGATCTGC 1629
CTTTGCTGCT CTGGACTTCG GGCTAATTAG GGACCACCGC TCGGGCTGTG TCTGTCTTGT 1689
TCTTCCACTA CTGGGGCGAG GGGGGCATTG GTCCCAGTCT CTGAGGTAGC CATGTCTGCC 1749
CATCTCCTGA GATTCTTGAT GATCCCAGCA CTCCACTGGT GGATGAAGGC ACTTATAGCC 1809
TGGGCATATT CTAGCACTGC AAAGTCATAG AAGGAATGTA CAGAAGGTGT TTTGGAACCT 1869
ATAAACCAAT GAAAATAAAA A 1890

```

## (2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 140 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```

Met Gln Cys Phe Lys Phe Ile Lys Val Met Met Ile Leu Phe Asn Leu
 1 5 10 15
Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
 20 25 30
Ser Val Asp Gly Thr Ser Phe Leu Lys Ala Phe Gly Ser Leu Ser Ser
 35 40 45
Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
 50 55 60

```

Ala Val Leu Phe Ile Leu Gly Phe Leu Gly Cys Tyr Gly Ala His Ser  
65 70 75 80

Glu Asn Lys Cys Val Leu Met Met Val Cys Trp Thr Gln Leu Pro Arg  
85 90 95

Pro Thr Thr Lys Gly Ser Pro Phe Ile Pro Asp Thr Ser Leu Trp Asp  
100 105 110

Pro Lys Thr Leu Leu Trp Ile Leu Glu Ala Ser Leu Trp Gly Pro Pro  
115 120 125

Ala Ser Tyr Gly Ser Val Gln Glu Gly Val Tyr Pro  
130 135 140

## (2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2181 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: HW083
- (ix) FEATURE:
  - (A) NAME/KEY: misc\_feature
  - (B) LOCATION: complement (1950..2181)
  - (D) OTHER INFORMATION: /label= SAC\_24528

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

|                                  |                                  |     |
|----------------------------------|----------------------------------|-----|
| GTCGACCCAC AATCGCCCGA GCACTTGGA  | TCACAGCAGA AACGACCCAA TCCTGAGCTC | 60  |
| CGTAGAAATG TGACCATCAA AACTGAACTC | CCACTAGGCG CACGGCGAAA GATGAAGCCA | 120 |
| CTGCTCCAC GGGTTAGCTC ATACCTGGTG  | CCCATCCAGT TCCCGGTGAA CCAGTCCCTG | 180 |
| GTGTTACAGC CCTCGGTGAA GGTTCCTTG  | CCTCTGGCAG CATCTCTTAT GAGCTCAGAG | 240 |
| CTTGCCCGTC ATAGCAAGCG AGTCCGCATT | GCACCCAAGG TGCTGCTATC CAACGAAGGG | 300 |
| ATAGCCCCAC TTCCTGCCAC AGAACCCATG | AAGGAGGAGA AACCCCTGCT TGGAGAAGGG | 360 |
| CTATTGCCTT TGCTTCCTAT TCAGTCCATT | AAGGAAGAAG TAATTCAGCC TGGGGAGGAC | 420 |
| ATACCACACT TAGAGAGGCC TATCAAAGTG | GAGAGCCCTC CCTTGGAAGA GTGGCCCTCT | 480 |
| CCGTGTGCAT CAGTGAAAGA GGAAGTGTCC | AACTCCTGGG AAGATTCTTC CTGCTCTCCT | 540 |
| ACCCCAAAGC CCAAGAAGTC CTATTGTGGG | CTTAAGTCCC CAACACGGTG TGTCTCAGAA | 600 |
| ATGCTGGTGA CAAAGCGGAG AGAGAAGAGA | GAGGTGAGCC GATCTCGGAG GAAGCAGCAC | 660 |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| CTTCAGCCAC CCTGTCTAGA TGAGCCTGAA CTCTTCTTCT CAGAGGACTC CAGCACATTT  | 720  |
| CGGCCAGCCA TGGAGATCCT GGCAGAGTCT TCAGAGCCTG CACCACAGCT CAGCTGCCCT  | 780  |
| CAGGAGGAGG GAGGGCCCTT CAAGACCCCC ATCAAGGAGA CATTGCCTGT CTCCTCCACT  | 840  |
| CCTAGCAAGT CTGTGCTCTC TAGAGACCCT GAGTCCTGGA GGCTCACACC CCCAGCCAAA  | 900  |
| GTTGGGGGGT TAGATTTTCA CCCAGTACGA ACCCCCCAGG GTGCCTTTGG CCCTCTGCCT  | 960  |
| GA CTCGCTGG GGCTTATGGA GCTGAATACC ACACCTCTGA AAAGTGTTC CCTCTTCGAC  | 1020 |
| TCACCCCGGG AGCTCCTTAA CTCAGAAGCC TTTGACCTTG CCTCTGATCC CTTTAGCAGT  | 1080 |
| TCTCCACCAC CACATTTGGA AGCCAAGCCA GGCTCCCCCG AGCTGCAGGT CCCCAGCCTT  | 1140 |
| TCAGCCAACC GTTCTCTCAC AGAAGGCCCTT GTCCTGGACA CAATGAATGA TAGCCTCAGC | 1200 |
| AAGATCCTTC TAGACATCAG TTTCCCTGGC CTGGAGGAGG ACCCTCTGGG CCCTGACAAC  | 1260 |
| ATCAACTGGT CTCAGTTTAT CCCTGAGCTG CGATAGAGGC AGGGTCTTAC CCTTGCCACT  | 1320 |
| CAAGCCACCA GTTATCCTGG CACTTGTGTG GCTGGATAGT GCAAGGCTCA GTGTACCCCA  | 1380 |
| AACCGTCTGA GGGAGCTAGC AGGCAAGGGC TGAGCGGTGC CCTTTGACCT AATTATGCCA  | 1440 |
| AGGTAAAAGC CACGTCTAAG CCACTGCTGG GACCTATGCA AGCAATAGGA TCTCCCAGAG  | 1500 |
| TCCTCCACTC CCTGCTGGCA AGTGAAGTGG GTGTGACAGA GCCGTGAGGA CCAGGAAATG  | 1560 |
| CCCACCCATT AGTCACCTGC TGCTCCTGGC AGGATAACCC TTGTAAATGG TGTCAGTTCC  | 1620 |
| CCAAGTTGTC CTGTAATTAT AAATGTAGCC ATATTCCCTT AGCTCTCATT ATCCAGAGAC  | 1680 |
| TGCCAGGATG GGTAGGGTGA CAAGGGGTTG CATTAGCTTC TGCTTGTGGC CTTTGGGGGC  | 1740 |
| AGGACCTGCA GTTCAGCCTC TTCACACTGT GGGTTCTGCT GTAGGCTTCT AGACACACAG  | 1800 |
| GTGTCTTTC CAGGACCCCA CTTACTGCCC TTTCTTCACA GCTCCCCCTG GTTCTAAGCC   | 1860 |
| AGTGGTACTG CATGAAGAAA TCCTGCGGCA AAGCCTATTG GCTCTGGGTG TGTGGGGACG  | 1920 |
| GGTGTGCCTG AAGCAAAAGC ATGGGTACTC ACGTGAGTCC TTTAGGTGTT TCTCTGATCG  | 1980 |
| TGTTCCCAAT CATGCCAGGG AGTCTAGCAT TGAGAACTCA GGCTGAGGCC TGAGGAGGAG  | 2040 |
| GAGGAAGTGA CCACTGACTT GCCTGGCTTC CTTAGCTTGC ACCTGAGTTT TGCAAAAAGC  | 2100 |
| CACCCTAGAC CCCACTCTAC AAGCTAGCAC AAGAACAATA CTGTAATACT CTAATACTGA  | 2160 |
| AAGCCAGGT GGCCTGAAAA A                                             | 2181 |

## (2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3336 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: HW084

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: complement (163..391)  
(D) OTHER INFORMATION: /label= SAC\_24854

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

|                                                                    |      |
|--------------------------------------------------------------------|------|
| TTTTTCCACC AAGAGGGAGT CCTTTAATAG ATTGCACAGA CAGACACAAC AGGCCAGCAC  | 60   |
| CCTGCTTGCA GGCCAGGCG CTTTGCCAGC AGATGCAATG GCCTCCCCCA CCTGGGTGTG   | 120  |
| GGCCGCAGGG TGGAGATGAG GTGGTTTAAA AAACACAGCT GTACTAATTC TTCACTTTCA  | 180  |
| CAGAAAAGAG AAACCTGGGG GAGCAGCTCA CAGGAGAATT TACATAGAGC TGAGTCTGAA  | 240  |
| TGTCCACCCC TAGAGAAGTT GAACCTCCCC CTGAGCTGTC TGTGCTCAGC AGGGGGCAGA  | 300  |
| CAGCACATGG AGGGCGCAGG CCAGTCCACA GAGGAGCGCT GACTTAAACA GCTGTCCTCC  | 360  |
| CTTCCCAGNT GTTAGNATTT CTACACNATG TACATTGTTG TGCTTTATTG CTCCCACCCC  | 420  |
| AGCCTCTGCC TGAAGCCCAG GGTGGAGGGA GGAACACCTG AACCAGATTC AGCTGGGTGG  | 480  |
| GAGCACCAAG CCCCCAATGG CTGGTGCTCT GTAAGNTTCT GAGGCTGCCA GGCTCNNGNC  | 540  |
| ACTCGGAGCT GCAGACCAAG GGTACAGAGC CAGCCGACCA GCCAGCTCTT CTGAGGAGCA  | 600  |
| GCAGAAACAG AAGGATCAGT GCTGGACAAG ATGCAGGCTG GGTAGGAGCA GGCAGGGTGG  | 660  |
| AAGGACGAGT GCAAGGCCAT GAGTCTGGGG CAGAGGGTTG TGCACATGGG GCTGTGGGGG  | 720  |
| CCTGCAGGGC ACCTCACGAG ACAGAACCAT TCTGTAGCAG AGCTTGACGG AGGAAGGGTG  | 780  |
| TGAGGACCAC TGGCCTGGGG CCCCTTGGAG CACAGAGCTG CTTCCAGTTC ATCAGGGGCT  | 840  |
| GGCAGTGGCA GGCCCCAGCT CGGGGCGTGT GCATTGGGAG ATTGAGGGAG AACCNCGAGG  | 900  |
| CAGCCTGTGG GGCTGGGTGA GGAGGGAAGG CTGTGGTGGT ATCTTTGAGT NTGTCTTGGC  | 960  |
| CGGGCCAGGG GTTAACACAG GATCAGTTGT TCTCAAAGAG TGAGAGCAGA TCATCACTGC  | 1020 |
| TGTTTGTGGG GAGGTCAGGT GGACCCAGGT AGGAGAGTAG TTCATCAGGA TTGGTCAGTT  | 1080 |
| CTGGGAGCAG ANCNAGAGCT GGTTCAGAGG CCTCCCCTGC CCCAGTCATG CTGGGAGGCC  | 1140 |
| CCATCATGCC CGTGGCAGNA TTGAAAGCCA GTTCACTGAT GGGCCCTGTG TTTGGTTGGC  | 1200 |
| CCAGGGGCTG CCTGGATGCA GGGGAAGGGT TTGGATGGTG TAGCTGGGTG CCTGGGGTGG  | 1260 |
| GGCCGAGGTT GGGAGTGTGC AGTCCTGGTG GTCCAGGATT ATGGGCTGGG TCCCAGGTGA  | 1320 |
| CCCTGCCTGG TGCCCATCCT GGCCCTGGGAG GCAAGGAGCA GACTTGNMNN GAGTCAGGAG | 1380 |
| GCTGCTGGGA ATGTCAGACT GGTAGGAGAT TGGGGGTGGC CCCTGGGGTG AACTCAGCAA  | 1440 |
| GGTTTGGGGT GGCGGGTGTA GCAGATGGGA AAGATTCTGG GAAGGTTCCA GGCCCCCAGG  | 1500 |

|            |             |            |            |            |             |      |
|------------|-------------|------------|------------|------------|-------------|------|
| AAGTTGGAAC | CCTGGCTGGG  | NTAGTCGNTG | GGGGTAGGGN | CCNAAGGGGC | TGCAATGGGG  | 1560 |
| CAAANGGGCA | GCGCCAGGGC  | CCAGGGCCGC | AATCATCTCC | ATCACACTGG | GCATGAGCAC  | 1620 |
| GTGGGCAGGG | CTCACAGTAC  | GGCAGCGCTT | CAGCACTGGG | CCCGTCCGGC | TCCTCCTTGA  | 1680 |
| TGTGTAGGTC | AGGCTTCACA  | GGCACTGGTT | TCCAGCTGCA | TGTGGGGTCG | ATGGTGATCT  | 1740 |
| CCTCGTAGTC | TGAGTTCTGA  | ATATAAATCA | GGATGCCTAG | CATATACTGA | TCCACCTCCA  | 1800 |
| GGCCCTCCAG | CAATGCCGTC  | TTGTTGCACA | CCGGGACACC | TCCAGGTCCC | CCGCTCACAG  | 1860 |
| TTAAGCTGTA | AGTATGACTC  | CAGGTCAAAG | CACTGTATGT | GGCGACAGTC | GTGACCACGA  | 1920 |
| GCTGGGAGCT | GGATCCTGCG  | GAAGGTGATG | GGGCACTTCA | GGGACACCTT | GATAGCCGTC  | 1980 |
| TGCTCCACCC | CATCCTCTCC  | ATTGGGCCCA | GGGGTGCCAG | GGATGGTGCC | GCTACTGAAG  | 2040 |
| TTCCGCTTTA | TCTTGGTGAT  | GCAGTGCTCA | GCTGGCAAGN | GGCGCTTCTT | GAGGAGACCC  | 2100 |
| TGCAGCACAG | AGCGGACAGA  | CGGACGGTGC | ACCAGCTGCA | GCACGAAGAG | GTGGGAGCAG  | 2160 |
| CAGCAGGCGG | TGACGGTGAT  | CTGGATGGTG | TTGCGACCCG | GCTGGCACAC | ATGCTTCAGG  | 2220 |
| TAGAGGGGCT | TGTGCGAGGT  | CTTGTTGTCT | CCACGCTCGA | TGCTGAGGGG | TGTGNCATTG  | 2280 |
| ACGCTGACCT | GCACCGNNGC  | CGGCCANTTG | GTGGTTCATC | TGCCGGTCCT | CGTGGTG GTA | 2340 |
| GCACTTGAAC | TGCGAACTGA  | GCTCTAAGTC | AGGTCTCAGC | ATCAGGGTTT | TATACACAGA  | 2400 |
| GTCTCGNAGC | TGGAAGACAT  | GGTTGCTCAC | AGCCAGGTTG | TGCTGCAGGC | GGAAGGGCTC  | 2460 |
| CAGGACCACC | CCATCCC GAA | CTGGGAAGGT | CAGGCGCAGC | TCGTACAGG  | GGACGCTTCC  | 2520 |
| AGAGGGTGAT | GGGTGCAAGG  | AGGCTGAGGC | CTGGCTTGAG | GTCAGGCAGG | AAAGGAGACT  | 2580 |
| TGACCTCCTG | GCTTGGGGAC  | ACGTAGGGAG | CACTGCTGCT | AGGCGTCATG | GGTGGTG TGG | 2640 |
| GATTCCCCGG | CAGTGGGGAG  | CTGGGGTAAG | CAGGGATGGA | GCGGGAAGGC | CCACTCAAGC  | 2700 |
| CAGGCTGGCT | GTAGCTGATG  | CTGCCCCCGT | TGAANCTGGC | GCCCTGCCCC | TTGAACTGCT  | 2760 |
| CTGTGGGCTT | GTAATGCAGN  | CCTGTGGGGC | CAGGGGCAGA | CAGGGACTGG | GCCATGCCCT  | 2820 |
| GCTGCAGGGG | GAGTCTGTGT  | CCTGCGTAGG | AGGAGGCAGG | GCCAGGGGGC | TGCCCCGGAC  | 2880 |
| CAGGAGCATA | CTGGGCAGTG  | CTGGCTGCAT | ACTGGCCNNC | TTGCAGATAT | TGNTGNCNAG  | 2940 |
| GATACACCTC | TGAGTAGGTC  | TCTCTTGACC | CNCTGTGAG  | GCAGCGGCTG | CCCCTGGGGA  | 3000 |
| GGCCCAGGGT | AGCCATGCTG  | AGGCAGTCGC | TGTCCTGCAT | ACAAGGGTGT | CATGCCTGCT  | 3060 |
| GCCCGTGTAG | GATTCATGGC  | CATGGAGGAA | AGGCCTGAGG | GGCCCATCAT | TCCTCCCATG  | 3120 |
| CCTGAAGGGT | TCATGCCAGG  | GGGTACACTG | GGCCCTCGAG | GACCTCCATG | CTGCAGAAAC  | 3180 |
| TGGCTGTTAA | AAGATTGCCC  | AGTCCCCATC | GCTCCATATT | GGCTTAGCTT | CCTGGCTCTN  | 3240 |
| CTTCTCTTGC | AGGGNNGCCA  | CAGTAGCTGT | GGCTGTGGCT | GTGGCCGTNC | TGCAGCAGCA  | 3300 |
| GCCATGGCAG | CTGCAGCTCT  | GCTTGTGTGA | AGTCAG     |            |             | 3336 |

## (2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1494 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: HW088

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 9..686

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: complement (612..909)  
 (D) OTHER INFORMATION: /label= SAC\_24336

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

|                                                                 |                                                         |    |
|-----------------------------------------------------------------|---------------------------------------------------------|----|
| GTCGACCC                                                        | GCT GCG GTC TAT CTG GGC AGC ACC ATG CTC GCG CTC CGA AGC | 50 |
|                                                                 | Ala Ala Val Tyr Leu Gly Ser Thr Met Leu Ala Leu Arg Ser |    |
|                                                                 | 1 5 10                                                  |    |
| GGC CTG AGG ACG GCG CTG GCC CCG CGG GCT CTG ACG CCT CAG GTA TGT | 98                                                      |    |
| Gly Leu Arg Thr Ala Leu Ala Pro Arg Ala Leu Thr Pro Gln Val Cys |                                                         |    |
| 15 20 25 30                                                     |                                                         |    |
| TCA CCT TTT GCT ACA GGC CCC AGG CAA AGC GAT GGG ACA TTG TAT GAA | 146                                                     |    |
| Ser Pro Phe Ala Thr Gly Pro Arg Gln Ser Asp Gly Thr Leu Tyr Glu |                                                         |    |
| 35 40 45                                                        |                                                         |    |
| TTC CGC ACC TAC TCT CTG AAG CCC TCA AAG ACA AAT GCG TTC CTG CAG | 194                                                     |    |
| Phe Arg Thr Tyr Ser Leu Lys Pro Ser Lys Thr Asn Ala Phe Leu Gln |                                                         |    |
| 50 55 60                                                        |                                                         |    |
| AAT TTT CAG AAA TAC GTT CAC CTT CGG ACA GCT CAC TCT GAG ATG ATT | 242                                                     |    |
| Asn Phe Gln Lys Tyr Val His Leu Arg Thr Ala His Ser Glu Met Ile |                                                         |    |
| 65 70 75                                                        |                                                         |    |
| GGA TAC TGG ACC GTA GAA TTT GGA GGC AAA ATA AAC AGA GTG TTC CAT | 290                                                     |    |
| Gly Tyr Trp Thr Val Glu Phe Gly Gly Lys Ile Asn Arg Val Phe His |                                                         |    |
| 80 85 90                                                        |                                                         |    |
| ATT TGG AAG TAT GAT AAT TTT GCT CAT CGA ACT GCC GTC CGC AAA GCC | 338                                                     |    |
| Ile Trp Lys Tyr Asp Asn Phe Ala His Arg Thr Ala Val Arg Lys Ala |                                                         |    |
| 95 100 105 110                                                  |                                                         |    |
| TTG GCC AAG GAT AAG GAA TGG CAA GAA CAA TTC CTC ATT TCA AAT TTG | 386                                                     |    |
| Leu Ala Lys Asp Lys Glu Trp Gln Glu Gln Phe Leu Ile Ser Asn Leu |                                                         |    |
| 115 120 125                                                     |                                                         |    |
| GCT TTC ATG GAT GAA CAA GAG GTT GAG ATT ACC TAC TTG GTA CCC TGG | 434                                                     |    |
| Ala Phe Met Asp Glu Gln Glu Val Glu Ile Thr Tyr Leu Val Pro Trp |                                                         |    |
| 130 135 140                                                     |                                                         |    |



|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| TGT AAA ATA AGA ACA CCT CCC AAG GAA GGA GTC TAT GAA CTG GCT ACC<br>Cys Lys Ile Arg Thr Pro Pro Lys Glu Gly Val Tyr Glu Leu Ala Thr<br>145 150 155     | 482  |
| TTT CAG ATG AAG CCT GGT GGC CCA GCT CTA TGG GGT GAT GCA TTC AAA<br>Phe Gln Met Lys Pro Gly Gly Pro Ala Leu Trp Gly Asp Ala Phe Lys<br>160 165 170     | 530  |
| AGG GCA ATA AAC GCC CAT GTT GAG CTT GGC TAC TCT ACA CTA GTT GGT<br>Arg Ala Ile Asn Ala His Val Glu Leu Gly Tyr Ser Thr Leu Val Gly<br>175 180 185 190 | 578  |
| GTT TTC CAC ACT GAA TAT GGA GCC CTC AAC AGA GTT CGG GAA AGT GTC<br>Val Phe His Thr Glu Tyr Gly Ala Leu Asn Arg Val Arg Glu Ser Val<br>195 200 205     | 626  |
| AAT TAC CTC GAG TCT CAG CAG AAT ATG TTC CTG ATT CCA ACC TCA TTT<br>Asn Tyr Leu Glu Ser Gln Gln Asn Met Phe Leu Ile Pro Thr Ser Phe<br>210 215 220     | 674  |
| TCA CCA TTG AAG TAGTTTCCTA CCGAGCGCTG AGCATTCCCA TCACGGAGGT<br>Ser Pro Leu Lys<br>225                                                                 | 726  |
| GAGATGCGTT TCCCCAGAC AATCGCCCTG TTCATTGTCT GAAGGAGGTG CTGAGCTACC                                                                                      | 786  |
| GCACTGCCCT CTGCATGTCT GAGACTTCAT GTATCCTTTA CTACCAGTCG CTCAGGAAAT                                                                                     | 846  |
| GTTCCTGTCC CTTTTCATGT CTACTGGATG TCAGAAAGTG GTGTTATTAC TCCATGCCCT                                                                                     | 906  |
| GGTACTTCAT TGTTCCTCTG TGGTTTTATG ATTAAGTCTT GTCCTCAAAA TATGATTTTG                                                                                     | 966  |
| AAATTTTTTC CCTCAAAATA TTTGGAAATT AAATAAATAC AATATCTGCC TTTTATTGCG                                                                                     | 1026 |
| GTTCATTTTC CCTGAAATTT TTAAGTGTGTT TTACCAGTAA TGTTTACTTT GTGATTTCAA                                                                                    | 1086 |
| ATGGGATTGA TAGAAGTCAG AGAAAGAACT GGAAGAGCTT GAAGGGGCTC GAGACCCCAT                                                                                     | 1146 |
| ATGTACAACA ATGCCAAGCA ACCAGAGCTT CCAGGGACTA AGCCACTACC TAAAGACTAT                                                                                     | 1206 |
| ACATGGACTG ACCCTGGACT CTGACCTCAT AGGTAGCAAT GAATATCCTA GTAAGAGCAC                                                                                     | 1266 |
| CAGTGAAGG GGAAGCCCTG GGTCTTGCTA AGACTGAACC CCAGTGAACG TGATTGTTGT                                                                                      | 1326 |
| GGGGAGAGTG GTAATGGGGG GAGGATGGGG AGGGGAAGCC CATATAGAAG GGGAGGGAGA                                                                                     | 1386 |
| GGGGTTAGGG GGATGTCGGC CCAGAAACCA GGAAGGGGAA TAACAATTGA AATGTAAATA                                                                                     | 1446 |
| AGAAATACTC AAGTTAATAA AGATGGAGAA AAGAAAAAGA AAGTCGAC                                                                                                  | 1494 |

## (2) INFORMATION FOR SEQ ID NO:77:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ala Ala Val Tyr Leu Gly Ser Thr Met Leu Ala Leu Arg Ser Gly Leu  
 1 5 10 15  
 Arg Thr Ala Leu Ala Pro Arg Ala Leu Thr Pro Gln Val Cys Ser Pro  
 20 25 30  
 Phe Ala Thr Gly Pro Arg Gln Ser Asp Gly Thr Leu Tyr Glu Phe Arg  
 35 40 45  
 Thr Tyr Ser Leu Lys Pro Ser Lys Thr Asn Ala Phe Leu Gln Asn Phe  
 50 55 60  
 Gln Lys Tyr Val His Leu Arg Thr Ala His Ser Glu Met Ile Gly Tyr  
 65 70 75 80  
 Trp Thr Val Glu Phe Gly Gly Lys Ile Asn Arg Val Phe His Ile Trp  
 85 90 95  
 Lys Tyr Asp Asn Phe Ala His Arg Thr Ala Val Arg Lys Ala Leu Ala  
 100 105 110  
 Lys Asp Lys Glu Trp Gln Glu Gln Phe Leu Ile Ser Asn Leu Ala Phe  
 115 120 125  
 Met Asp Glu Gln Glu Val Glu Ile Thr Tyr Leu Val Pro Trp Cys Lys  
 130 135 140  
 Ile Arg Thr Pro Pro Lys Glu Gly Val Tyr Glu Leu Ala Thr Phe Gln  
 145 150 155 160  
 Met Lys Pro Gly Gly Pro Ala Leu Trp Gly Asp Ala Phe Lys Arg Ala  
 165 170 175  
 Ile Asn Ala His Val Glu Leu Gly Tyr Ser Thr Leu Val Gly Val Phe  
 180 185 190  
 His Thr Glu Tyr Gly Ala Leu Asn Arg Val Arg Glu Ser Val Asn Tyr  
 195 200 205  
 Leu Glu Ser Gln Gln Asn Met Phe Leu Ile Pro Thr Ser Phe Ser Pro  
 210 215 220  
 Leu Lys  
 225

## (2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1082 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

- (B) CLONE: HW089

(ix) FEATURE:

- (A) NAME/KEY: CDS

(B) LOCATION: 8..1006

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature

(B) LOCATION: 961..1076

(D) OTHER INFORMATION: /label= SAC\_24461

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

|         |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GTCGACC | AAG | CAA | CAG | CAG | GGA | AGT | GAA | TTT | CAG | ACA | CTG | CTG | GAG | GCT | 49  |     |
|         | Lys | Gln | Gln | Gln | Gly | Ser | Glu | Phe | Gln | Thr | Leu | Leu | Glu | Ala |     |     |
| 1       |     |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     |     |
| GAG     | GAG | ACC | AAA | GCC | GCC | TCT | GAC | GCT | TCA | AAT | AAA | AAG | CTT | TGG | TCC | 97  |
| Glu     | Glu | Thr | Lys | Ala | Ala | Ser | Asp | Ala | Ser | Asn | Lys | Lys | Leu | Trp | Ser |     |
| 15      |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| CTC     | AGA | ACT | CTA | CCC | TTC | CAG | CCC | TGC | TCT | GAA | GCC | TCA | GAC | GTG | AGA | 145 |
| Leu     | Arg | Thr | Leu | Pro | Phe | Gln | Pro | Cys | Ser | Glu | Ala | Ser | Asp | Val | Arg |     |
|         |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| ACC     | ATG | TCT | GTG | ACC | CTG | CAA | GCT | GTC | CTC | TAC | AGT | CTT | CAG | GAG | GAG | 193 |
| Thr     | Met | Ser | Val | Thr | Leu | Gln | Ala | Val | Leu | Tyr | Ser | Leu | Gln | Glu | Glu |     |
|         |     |     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |
| CAG     | TCC | AGG | CTC | AAG | ACG | AGG | CTG | CAG | GAA | CTA | CAG | CAG | CTG | AAA | AGG | 241 |
| Gln     | Ser | Arg | Leu | Lys | Thr | Arg | Leu | Gln | Glu | Leu | Gln | Gln | Leu | Lys | Arg |     |
|         |     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     |     |
| GAG     | CGC | ATA | GAT | GTT | CCC | AGA | GAC | AAG | ATC | CCA | TTC | CCG | GTG | CCT | GAA | 289 |
| Glu     | Arg | Ile | Asp | Val | Pro | Arg | Asp | Lys | Ile | Pro | Phe | Pro | Val | Pro | Glu |     |
|         | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |
| GTC     | CCC | GTG | GTA | TTC | CAA | GGT | CTA | ACT | AAG | CAG | AGC | GGC | CAA | GCA | CCC | 337 |
| Val     | Pro | Val | Val | Phe | Gln | Gly | Leu | Thr | Lys | Gln | Ser | Gly | Gln | Ala | Pro |     |
| 95      |     |     |     | 100 |     |     |     |     | 105 |     |     |     |     |     | 110 |     |
| AAG     | TCT | CTA | GTT | TCT | AAC | TTG | AAG | ATC | TGC | TGC | CCT | CTG | CCT | GGA | GGT | 385 |
| Lys     | Ser | Leu | Val | Ser | Asn | Leu | Lys | Ile | Cys | Cys | Pro | Leu | Pro | Gly | Gly |     |
|         |     |     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |
| TCT     | GCT | CTG | ATC | ACC | TTT | GAT | GAC | CCC | AAA | GTG | GTT | GAG | CGG | TTG | CTA | 433 |
| Ser     | Ala | Leu | Ile | Thr | Phe | Asp | Asp | Pro | Lys | Val | Val | Glu | Arg | Leu | Leu |     |
|         |     |     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |
| CAA     | CAA | AAG | GAA | CAT | AAA | GTT | GAC | ATC | GAG | GAC | TGC | CGG | CTG | CGG | GTG | 481 |
| Gln     | Gln | Lys | Glu | His | Lys | Val | Asp | Ile | Glu | Asp | Cys | Arg | Leu | Arg | Val |     |
|         |     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     |     |
| CAG     | ATC | CAG | CCC | TTG | GAG | CTG | CCT | ATG | GTG | ACC | AAC | ATC | CAG | GTG | TCC | 529 |
| Gln     | Ile | Gln | Pro | Leu | Glu | Leu | Pro | Met | Val | Thr | Asn | Ile | Gln | Val | Ser |     |
|         | 160 |     |     |     | 165 |     |     |     |     |     | 170 |     |     |     |     |     |
| AGC     | CAG | CCG | GAT | AGC | CAC | AGG | GTG | CTA | GTC | AGT | GGC | TTT | CCT | ACT | GGA | 577 |
| Ser     | Gln | Pro | Asp | Ser | His | Arg | Val | Leu | Val | Ser | Gly | Phe | Pro | Thr | Gly |     |
| 175     |     |     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |
| CTT     | AGG | CTG | AGT | GAG | GAG | GAG | CTA | CTG | GAC | AAG | TTA | GAG | ATC | TTC | TTC | 625 |
| Leu     | Arg | Leu | Ser | Glu | Glu | Glu | Leu | Leu | Asp | Lys | Leu | Glu | Ile | Phe | Phe |     |
|         |     |     | 195 |     |     |     |     | 200 |     |     |     |     |     | 205 |     |     |
| GGC     | AAG | GCC | AAG | AAT | GGA | GGT | GGG | GAT | GTG | GAG | ACC | CGG | GAG | ATG | CTG | 673 |

|                                                                  |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
|------------------------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Gly                                                              | Lys | Ala | Lys | Asn | Gly | Gly | Gly | Asp | Val | Glu | Thr | Arg | Glu | Met | Leu |      |  |
|                                                                  |     |     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |      |  |
| CAA                                                              | GGG | ACT | GTC | ATG | CTG | GGA | TTT | GCT | AAT | GAA | GAA | GTG | GCC | CAG | CAC | 721  |  |
| Gln                                                              | Gly | Thr | Val | Met | Leu | Gly | Phe | Ala | Asn | Glu | Glu | Val | Ala | Gln | His |      |  |
|                                                                  |     | 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |      |  |
| TTA                                                              | TGC | CAG | ATT | GGC | CAG | TTC | AGA | GTC | CCA | CTG | GGT | CGG | CAG | CAG | GTC | 769  |  |
| Leu                                                              | Cys | Gln | Ile | Gly | Gln | Phe | Arg | Val | Pro | Leu | Gly | Arg | Gln | Gln | Val |      |  |
|                                                                  | 240 |     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     |      |  |
| CTT                                                              | TTG | AGG | GTC | TCT | CCC | TAT | GTG | AGT | GGG | GAG | ATC | CAG | GAA | GCT | GAG | 817  |  |
| Leu                                                              | Leu | Arg | Val | Ser | Pro | Tyr | Val | Ser | Gly | Glu | Ile | Gln | Glu | Ala | Glu |      |  |
| 255                                                              |     |     |     |     | 260 |     |     |     |     | 265 |     |     |     |     | 270 |      |  |
| ATC                                                              | AAA | TTC | CAG | CAA | GCA | CCT | CAT | TCA | GTG | CTG | GTG | ACG | AAT | ATT | CCC | 865  |  |
| Ile                                                              | Lys | Phe | Gln | Gln | Ala | Pro | His | Ser | Val | Leu | Val | Thr | Asn | Ile | Pro |      |  |
|                                                                  |     |     | 275 |     |     |     |     | 280 |     |     |     |     |     | 285 |     |      |  |
| GAC                                                              | GTC | CTG | GAT | GTG | CAG | GAA | CTG | CAT | GAC | ATT | CTG | GAG | ATC | CAC | TTC | 913  |  |
| Asp                                                              | Val | Leu | Asp | Val | Gln | Glu | Leu | His | Asp | Ile | Leu | Glu | Ile | His | Phe |      |  |
|                                                                  |     |     | 290 |     |     |     |     | 295 |     |     |     |     | 300 |     |     |      |  |
| CAG                                                              | AAG | CCT | ACC | CGT | GGG | GGC | GGA | GAG | GTG | GAG | GCC | CTG | GCA | GTT | GTA | 961  |  |
| Gln                                                              | Lys | Pro | Thr | Arg | Gly | Gly | Gly | Glu | Val | Glu | Ala | Leu | Ala | Val | Val |      |  |
|                                                                  |     | 305 |     |     |     | 310 |     |     |     |     |     | 315 |     |     |     |      |  |
| CCT                                                              | GTG | GGG | CAG | CAG | GGC | CTG | GCT | GTC | TTT | ACT | TCT | GAG | TCA | AGC |     | 1006 |  |
| Pro                                                              | Val | Gly | Gln | Gln | Gly | Leu | Ala | Val | Phe | Thr | Ser | Glu | Ser | Ser |     |      |  |
|                                                                  | 320 |     |     |     |     | 325 |     |     |     |     | 330 |     |     |     |     |      |  |
| TAGGGCTGCA TGTCACCTG CTGGGCATGG GACTGCTCAT TGCCTAATGC TACCAAGAAC |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 1066 |  |
| AGTGAAAGGC GTCGAC                                                |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     | 1082 |  |

## (2) INFORMATION FOR SEQ ID NO:79:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |  |  |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Lys | Gln | Gln | Gln | Gly | Ser | Glu | Phe | Gln | Thr | Leu | Leu | Glu | Ala | Glu | Glu |  |  |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |  |  |
| Thr | Lys | Ala | Ala | Ser | Asp | Ala | Ser | Asn | Lys | Lys | Leu | Trp | Ser | Leu | Arg |  |  |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |  |  |
| Thr | Leu | Pro | Phe | Gln | Pro | Cys | Ser | Glu | Ala | Ser | Asp | Val | Arg | Thr | Met |  |  |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |  |  |
| Ser | Val | Thr | Leu | Gln | Ala | Val | Leu | Tyr | Ser | Leu | Gln | Glu | Glu | Gln | Ser |  |  |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |  |  |
| Arg | Leu | Lys | Thr | Arg | Leu | Gln | Glu | Leu | Gln | Gln | Leu | Lys | Arg | Glu | Arg |  |  |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     | 80  |     |  |  |
| Ile | Asp | Val | Pro | Arg | Asp | Lys | Ile | Pro | Phe | Pro | Val | Pro | Glu | Val | Pro |  |  |

| 85         |            |            |            |            |            |            |            | 90         |            |            |            | 95         |            |            |            |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Val        | Val        | Phe        | Gln<br>100 | Gly        | Leu        | Thr        | Lys        | Gln<br>105 | Ser        | Gly        | Gln        | Ala        | Pro<br>110 | Lys        | Ser        |
| Leu        | Val        | Ser<br>115 | Asn        | Leu        | Lys        | Ile        | Cys<br>120 | Cys        | Pro        | Leu        | Pro        | Gly<br>125 | Gly        | Ser        | Ala        |
| Leu        | Ile<br>130 | Thr        | Phe        | Asp        | Asp        | Pro<br>135 | Lys        | Val        | Val        | Glu        | Arg<br>140 | Leu        | Leu        | Gln        | Gln        |
| Lys<br>145 | Glu        | His        | Lys        | Val        | Asp<br>150 | Ile        | Glu        | Asp        | Cys        | Arg<br>155 | Leu        | Arg        | Val        | Gln        | Ile<br>160 |
| Gln        | Pro        | Leu        | Glu        | Leu<br>165 | Pro        | Met        | Val        | Thr        | Asn<br>170 | Ile        | Gln        | Val        | Ser        | Ser<br>175 | Gln        |
| Pro        | Asp        | Ser        | His<br>180 | Arg        | Val        | Leu        | Val        | Ser<br>185 | Gly        | Phe        | Pro        | Thr        | Gly<br>190 | Leu        | Arg        |
| Leu        | Ser        | Glu<br>195 | Glu        | Glu        | Leu        | Leu        | Asp<br>200 | Lys        | Leu        | Glu        | Ile        | Phe<br>205 | Phe        | Gly        | Lys        |
| Ala        | Lys<br>210 | Asn        | Gly        | Gly        | Gly        | Asp<br>215 | Val        | Glu        | Thr        | Arg        | Glu<br>220 | Met        | Leu        | Gln        | Gly        |
| Thr<br>225 | Val        | Met        | Leu        | Gly        | Phe<br>230 | Ala        | Asn        | Glu        | Glu        | Val<br>235 | Ala        | Gln        | His        | Leu        | Cys<br>240 |
| Gln        | Ile        | Gly        | Gln        | Phe<br>245 | Arg        | Val        | Pro        | Leu        | Gly<br>250 | Arg        | Gln        | Gln        | Val        | Leu<br>255 | Leu        |
| Arg        | Val        | Ser        | Pro<br>260 | Tyr        | Val        | Ser        | Gly        | Glu<br>265 | Ile        | Gln        | Glu        | Ala        | Glu<br>270 | Ile        | Lys        |
| Phe        | Gln        | Gln<br>275 | Ala        | Pro        | His        | Ser        | Val<br>280 | Leu        | Val        | Thr        | Asn        | Ile<br>285 | Pro        | Asp        | Val        |
| Leu        | Asp<br>290 | Val        | Gln        | Glu        | Leu        | His<br>295 | Asp        | Ile        | Leu        | Glu        | Ile<br>300 | His        | Phe        | Gln        | Lys        |
| Pro<br>305 | Thr        | Arg        | Gly        | Gly        | Gly<br>310 | Glu        | Val        | Glu        | Ala        | Leu<br>315 | Ala        | Val        | Val        | Pro        | Val<br>320 |
| Gly        | Gln        | Gln        | Gly        | Leu<br>325 | Ala        | Val        | Phe        | Thr        | Ser<br>330 | Glu        | Ser        | Ser        |            |            |            |

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2263 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: HW090

## (ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 335..937

## (ix) FEATURE:

(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1355..1434  
(D) OTHER INFORMATION: /label= SAC\_24197

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

GTCGACCTTT AAGCTTACCA TCAGAACAAC AAATCAAAAT GTAAACTTAA AATATAACCA 60
AAAGAGGGAC AGCTCTTTAG GAAAAGGAAA AAACCTTAAA TAGTGAATAA ACAACTACAA 120
CCACTTAACC ATTGTAGGCT TAAAAGCAGC CATCAATAAA GAAAGCGTTC AAGCTCAACA 180
TACACACACA CACACACACA CACACACGCT CCCTCCCTCC GCGCCTCTAC TCCGCGCCCG 240
CCCGCCCGCT CGCCCGCCCG CCCGCCCTCGC ACGCACCGGC CTCGGCTCCC CGCGCCCGCC 300
GCCGAGCGAA GCTGCTCTGG GATCGGAGCA GCTC ATG GAG AAA GTG CCG GGC 352
 Met Glu Lys Val Pro Gly
 1 5

GAC ATG GAG ATA GAG CGC AGG GAG AGG AAC GAG GAG CTG TCC GAG GCG 400
Asp Met Glu Ile Glu Arg Arg Glu Arg Asn Glu Glu Leu Ser Glu Ala
 10 15 20

GAG AGG AAG GCG GTT CAG GCT ACG TGG GCC CGG CTG TAT GCC AAC TGC 448
Glu Arg Lys Ala Val Gln Ala Thr Trp Ala Arg Leu Tyr Ala Asn Cys
 25 30 35

GAG GAC GTG GGG GTG GCC ATC CTG GTG AGG TTC TTT GTG AAC TTC CCG 496
Glu Asp Val Gly Val Ala Ile Leu Val Arg Phe Phe Val Asn Phe Pro
 40 45 50

TCG GCC AAG CAG TAC TTC AGC CAG TTT AAA CAC ATG GAG GAT CCG TTG 544
Ser Ala Lys Gln Tyr Phe Ser Gln Phe Lys His Met Glu Asp Pro Leu
 55 60 65 70

GAG ATG GAG AGG AGT CCT CAG CTG CGG AAA CAT GCC TGC CGG GTC ATG 592
Glu Met Glu Arg Ser Pro Gln Leu Arg Lys His Ala Cys Arg Val Met
 75 80 85

GGG GCC CTC AAC ACG GTC GTG GAG AAC CTG CAT GAC CCA GAC AAG GTA 640
Gly Ala Leu Asn Thr Val Val Glu Asn Leu His Asp Pro Asp Lys Val
 90 95 100

TCC TCT GTG CTC GCG CTG GTT GGC AAG GCC CAC GCC CTC AAG CAC AAG 688
Ser Ser Val Leu Ala Leu Val Gly Lys Ala His Ala Leu Lys His Lys
 105 110 115

GTG GAA CCT ATG TAC TTT AAG ATT CTC TCT GGG GTC ATT CTG GAC GTG 736
Val Glu Pro Met Tyr Phe Lys Ile Leu Ser Gly Val Ile Leu Asp Val
 120 125 130

ATC GCC GAG GAG TTT GCC AAT GAC TTC CCC GTC GAG ACG CAG AAA GCC 784
Ile Ala Glu Glu Phe Ala Asn Asp Phe Pro Val Glu Thr Gln Lys Ala
 135 140 145 150

TGG ACC AAG CTG CGC GGT CTC ATC TAC AGC CAT GTG ACC GCG GCC TAC 832

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|                                                                   |      |
|-------------------------------------------------------------------|------|
| Trp Thr Lys Leu Arg Gly Leu Ile Tyr Ser His Val Thr Ala Ala Tyr   |      |
| 155 160 165                                                       |      |
| AAG GAA GTG GGC TGG GTA CAG CAG CCT ACC AGC CAC ACT GCC CTC TTC   | 880  |
| Lys Glu Val Gly Trp Val Gln Gln Pro Thr Ser His Thr Ala Leu Phe   |      |
| 170 175 180                                                       |      |
| AGG GCC ATA GGA CCC CTC CCA GCT CCC CCC TCC CTG GCA GCA CTT TGG   | 928  |
| Arg Ala Ile Gly Pro Leu Pro Ala Pro Pro Ser Leu Ala Ala Leu Trp   |      |
| 185 190 195                                                       |      |
| GCA GAA GGC TGA CTCTCTGA AGACACTCCT TGACCTTCCA TTTCTGGGTG         | 977  |
| Ala Glu Gly                                                       |      |
| 200                                                               |      |
| CCAAGGAAGC TGGAGGAACC CCTGACTGGA CTTCCCGAAA GGAGGCCTTC ATCATGGCTG | 1037 |
| TGGTCTCCCA CGTTACTGGG AGGTGGGGCT GGCTACCTGG ATGCTGAATT TAGCAGAGGG | 1097 |
| GAACCTTTCT GCCTCGCAGC AGAGGGCACA CCCTCCTTAG CTTTCACTGT CAAGAGAGGG | 1157 |
| ACCTGGCATG TGGCCGGTGG GAAGCAAGGA CAAGCCTTTG AGTCACTTCA GAAAGGAACT | 1217 |
| AGCCCTGCTT CACTCTGCCC TACCAGCATG CAGGTTCTCC TCACCATCTC TGAGCATTGC | 1277 |
| GCACACACAC GTCTACCATA TACACAGATA TATTCTATAT ACGAGCTCTA TATAAATATA | 1337 |
| TATACACACA CACACGTACA TATCTGTGCG GTGCACCTGC AGGCCAGAA GCCTAGGCCT  | 1397 |
| CGCACAGCTG TGGGAGACCC GGAAGAGTCC TGGCCGTA CTAGGGCAGC TCTACCGGA    | 1457 |
| GCAGGGAGAA AGCTTGCAAC AGCACGAGAG GCGGGGGCCG GGTGGGAGAG TCGGGGTGAC | 1517 |
| TCAGCTCACC CCGCACAGCT CAGTGCCCTG CAATCTTCCC CTTCCGCCCC CCAAAGAGA  | 1577 |
| ACACTTGGTT TGCCCGGTGT CGGGGCGCAC ACCTGTAATC CCCGAGTTTG GGACGCAGAG | 1637 |
| GAAGGACAAT CTTTGCAAGT CTGAGGTCAG GTGGTCTACA CTTGGTCTCC ATCTTGGTGA | 1697 |
| GTTTCCGGCT AGCTGGGGTC GACTCAGGGA GACCCCGTGT CAAACAAAAC AAGAAGCGAA | 1757 |
| GAGAAGATCT GGCTCCCCTC CCCTCCCCAA GGGTTTGCCC GACTGACTTG CTCCGGAAG  | 1817 |
| GGGCACACCG AGAATTCAGG AGACCCAGT GGGGTGCTGG CCAGTGTAGG TGTCCGGCGT  | 1877 |
| TTGGGGGTGG GGTGAGGGGC AGCTTCAGCG TGGAGCCCTA GAATGTCAGC CTCACCCGCT | 1937 |
| CACTTCAGAC AGCAGCCAGG CCACAGGACC AGGGGCCATA CTCAAACCCC TCAGCAGAGA | 1997 |
| CCAGGGCGCC TCTCTCCTGC CCTCCTCGGG GCCACCTGCC CATCCTCTCC AACTAGTCTC | 2057 |
| CGTAACATTC GCTGGGGACC CCGTGTGTAC CCCTTGGTCA CGTGTACTGT CCTGGAGGAC | 2117 |
| GTCTTACTGC TGTGGCTACC GTGCCTGCGT CCCCTCTGGT CCCACCCTCA CGCAGCCTTC | 2177 |
| CTGTAACTGC CTGTCTTTTT GTAGTTTCTG ATGTTTGTA CCAGACCCAG CTGTGTCATT  | 2237 |
| AAACAGGTCT GTTCTTCCTG TAAAAA                                      | 2263 |

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```

Met Glu Lys Val Pro Gly Asp Met Glu Ile Glu Arg Arg Glu Arg Asn
 1 5 10 15
Glu Glu Leu Ser Glu Ala Glu Arg Lys Ala Val Gln Ala Thr Trp Ala
 20 25 30
Arg Leu Tyr Ala Asn Cys Glu Asp Val Gly Val Ala Ile Leu Val Arg
 35 40 45
Phe Phe Val Asn Phe Pro Ser Ala Lys Gln Tyr Phe Ser Gln Phe Lys
 50 55 60
His Met Glu Asp Pro Leu Glu Met Glu Arg Ser Pro Gln Leu Arg Lys
 65 70 75 80
His Ala Cys Arg Val Met Gly Ala Leu Asn Thr Val Val Glu Asn Leu
 85 90 95
His Asp Pro Asp Lys Val Ser Ser Val Leu Ala Leu Val Gly Lys Ala
100 105 110
His Ala Leu Lys His Lys Val Glu Pro Met Tyr Phe Lys Ile Leu Ser
115 120 125
Gly Val Ile Leu Asp Val Ile Ala Glu Glu Phe Ala Asn Asp Phe Pro
130 135 140
Val Glu Thr Gln Lys Ala Trp Thr Lys Leu Arg Gly Leu Ile Tyr Ser
145 150 155 160
His Val Thr Ala Ala Tyr Lys Glu Val Gly Trp Val Gln Gln Pro Thr
165 170 175
Ser His Thr Ala Leu Phe Arg Ala Ile Gly Pro Leu Pro Ala Pro Pro
180 185 190
Ser Leu Ala Ala Leu Trp Ala Glu Gly
195 200

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(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1740 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: HW092



## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature  
 (B) LOCATION: complement (303..566)  
 (D) OTHER INFORMATION: /label= SAC\_24320

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

|             |            |            |            |            |            |      |
|-------------|------------|------------|------------|------------|------------|------|
| GTCGACCTCG  | GAGCTGGGGA | CCGAACCCAG | GGCCTTGCGC | TTGCTAGGCA | AGCGCTCTAC | 60   |
| CACTGAGCTA  | AATCCCCAAC | CCCTAGCCCT | TTGTTTTTTA | AGAAAGTCTA | GTGTAGCCCA | 120  |
| GGTTGGCCTT  | AAATTCCTGA | TCCTCCTGCC | CCTATCTGTA | ATCTTGGGAT | TATAGGTGTG | 180  |
| GGCCATCACA  | CTGTTTATCC | AGTGCTGAAT | CAAACCCAGA | ATCTTCCACA | TGCTAGGCGA | 240  |
| GCAGTCTCCT  | AAATACTACA | CGGCTATAGG | TTCAGCCTAG | ATCTCTCTTT | TGAAGCTCTC | 300  |
| GTACACCTAT  | AGGGGCCACT | AATCCTAAAG | ACGCAGAGGA | TGAAAACCAC | CAGGCCCAAG | 360  |
| GGTTAACGTG  | GAAAACAGAG | CCCTGGTGTC | CCCCTGGGGA | ACCAGCCCTT | CATGTTCTAA | 420  |
| GACAGTCATC  | ACCCAGATTC | CTGAAAACAA | TAGCGGCTTC | TTGTTTAGAA | CGGAACCGCA | 480  |
| CCTGCTGGAA  | TACGTGTCAA | CAAACAATCG | CTTGTTTTTT | CATATTCGCC | ATCCAAGCTG | 540  |
| AGGCAATGGG  | ACTTCCTGAA | GCGAGTACTG | GAAGACTTAT | TCTTAGAAGA | GGACAGAATT | 600  |
| CTCATTTTTAA | CACGAGGCTC | AGGGGCCGAG | TGCTGGCCAT | CTTCCTTCCT | TCTTTTGTAC | 660  |
| TCCCTGGTGT  | TCATCTTATT | TGGTTTTCAA | CAGGTTTATT | TCCATTGCAG | CCCGGGGCTT | 720  |
| CCAACGCCCA  | AAAACGCCCA | GCCCACGATG | CCGTAAATGG | TGAGCACGCT | GGCTTCTGCT | 780  |
| TCCTCTCCCT  | GAGAACCCAG | ACCTTTGTGT | GTTCGCCCAT | TCCAAAAGGC | CCTGGGAAGG | 840  |
| TTCTTTGCTC  | CTCTGGTGAC | AGGCTTGGGA | TGAAGACTTG | GGAACTCCTA | TTTGCTAAAC | 900  |
| TCTCGCTCCT  | GGCTAAATCT | TTCTGCTTGT | TCTTTTTCCT | CGTCTAATCA | TGCTACCTGC | 960  |
| TACTACTTTT  | CCTGATGCAG | TCTGACGAAC | GTCTGTTGAA | CACATCGGGA | CAGTTTTTAA | 1020 |
| AGGAGTTATT  | TTGGTGCCAA | AGGCGCTCAG | TTGTGATTTA | AAAGTGTTTT | AAGTGATTCA | 1080 |
| TCCAAGGTTG  | TCTCCATGGA | CTCCGAAAT  | AACCACAGCC | AAAATACCCC | GGCGAGAGCA | 1140 |
| GAATATGAGA  | GGCAGATAGC | ACCTATTATT | ACTTTTATCT | GGGTGCAGCC | GGGCTCCAGA | 1200 |
| TTAATGGGGG  | CAAGCAAAGG | TCCAGGCCTC | AGACATGGCC | AATTTTAAGC | AAACTAGTGC | 1260 |
| TAGTGTGTGAT | AAGTATTCAA | TAAGGGCTTG | GAATCTAATT | ATTTGTAAGA | AGTGTCTTTG | 1320 |
| TTTCCTGATC  | TGTAAAGGAG | ATGGGGAAAT | ACTGTGATTT | CGTGCCATTT | TAAAAAAAAT | 1380 |
| GAAAAAGCAA  | CATAAAAAAA | TGCAAATACA | GAAGAAAAGA | TGTGGGGTTT | GAAGTTGGCT | 1440 |
| TTAGAGAGCT  | GTGTAACCTT | GGGGAAGTCA | CCTCGTCTCT | CTGTGACTTG | AATTCCTAAT | 1500 |
| CAACAATAAT  | GCTGGGGGAC | AAGGTGCTCT | CCAAATTCCC | CTTCAGATCA | GAAAGTCTGG | 1560 |
| GATAACTATC  | CCAGATAGAT | CCAACTTGT  | AAAGGAATCA | AAAGGAATAG | TCTAGTGTGA | 1620 |
| CAGATAACAC  | GGACTTGAAA | CTTAGTTCAC | CTGATATTTT | TTAATGACTT | AACACCACTA | 1680 |

TACCTCACCC CAGAGCTAGC CTGTCCCCTG TGTGCCACC AGTAACCTTG AAATGTCGAC 1740

(2) INFORMATION FOR SEQ ID NO:83:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1385 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: HW093

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 8..1357

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: 798..1385  
 (D) OTHER INFORMATION: /label= SAC\_24538

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

|         |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| GTCGACT | CTG | CCT | CAG | CCG | CTG | CCG | CCG | CCA | CTG | CTG | CTG | CAG | GAT | CCG | 49  |     |
|         | Leu | Pro | Gln | Pro | Leu | Pro | Pro | Pro | Leu | Leu | Leu | Gln | Asp | Pro |     |     |
|         | 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     |     |     |
| CCG     | CAG | CCA | CCA | GTC | TCG | CGC | GTC | GTC | GCT | CCC | TCC | TTG | GAC | AGT | AAT | 97  |
| Pro     | Gln | Pro | Pro | Val | Ser | Arg | Val | Val | Ala | Pro | Ser | Leu | Asp | Ser | Asn |     |
| 15      |     |     |     | 20  |     |     |     |     | 25  |     |     |     |     |     | 30  |     |
| TTT     | ATG | AAT | AAG | CAT | CAG | AAG | CCG | GTA | CTA | ACA | GGC | CAG | CGG | TTC | AAA | 145 |
| Phe     | Met | Asn | Lys | His | Gln | Lys | Pro | Val | Leu | Thr | Gly | Gln | Arg | Phe | Lys |     |
|         |     |     |     | 35  |     |     |     | 40  |     |     |     |     |     | 45  |     |     |
| ACC     | CGG | AAA | AGG | GAT | GAA | AAA | GAG | AAA | TTC | GAA | CCC | ACA | GTC | TTC | AGG | 193 |
| Thr     | Arg | Lys | Arg | Asp | Glu | Lys | Glu | Lys | Phe | Glu | Pro | Thr | Val | Phe | Arg |     |
|         |     |     | 50  |     |     |     | 55  |     |     |     |     |     | 60  |     |     |     |
| GAT     | ACA | CTT | GTC | CAG | GGG | CTT | AAT | GAA | GCT | GGT | GAT | GAC | CTT | GAA | GCT | 241 |
| Asp     | Thr | Leu | Val | Gln | Gly | Leu | Asn | Glu | Ala | Gly | Asp | Asp | Leu | Glu | Ala |     |
|         |     |     | 65  |     |     | 70  |     |     |     |     |     | 75  |     |     |     |     |
| GTA     | GCC | AAA | TTC | TTG | GAC | TCT | ACT | GGC | TCA | CGA | CTA | GAT | TAT | CGT | CGC | 289 |
| Val     | Ala | Lys | Phe | Leu | Asp | Ser | Thr | Gly | Ser | Arg | Leu | Asp | Tyr | Arg | Arg |     |
|         | 80  |     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     |
| TAT     | GCA | GAC | ACA | CTC | TTT | GAT | ATC | CTG | GTG | GCT | GGC | AGC | ATG | CTT | GCC | 337 |
| Tyr     | Ala | Asp | Thr | Leu | Phe | Asp | Ile | Leu | Val | Ala | Gly | Ser | Met | Leu | Ala |     |
|         | 95  |     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |
| CCT     | GGA | GGA | ACA | CGC | ATA | GAT | GAT | GGT | GAC | AAG | ACC | AAG | ATG | ACC | AAC | 385 |
| Pro     | Gly | Gly | Thr | Arg | Ile | Asp | Asp | Gly | Asp | Lys | Thr | Lys | Met | Thr | Asn |     |
|         |     |     |     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |

|                   |            |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |                   |            |                   |      |
|-------------------|------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|------------|-------------------|------|
| CAC<br>His        | TGT<br>Cys | GTG<br>Val        | TTT<br>Phe<br>130 | TCA<br>Ser        | GCA<br>Ala        | AAT<br>Asn        | GAA<br>Glu<br>135 | GAT<br>Asp<br>135 | CAT<br>His        | GAA<br>Glu        | ACC<br>Thr        | ATC<br>Ile<br>140 | CGA<br>Arg<br>140 | AAC<br>Asn | TAT<br>Tyr        | 433  |
| GCT<br>Ala        | CAG<br>Gln | GTG<br>Val<br>145 | TTT<br>Phe        | AAC<br>Asn        | AAA<br>Lys        | CTC<br>Leu        | ATC<br>Ile<br>150 | AGG<br>Arg        | AGA<br>Arg        | TAC<br>Tyr        | AAA<br>Lys        | TAT<br>Tyr<br>155 | TTG<br>Leu        | GAA<br>Glu | AAG<br>Lys        | 481  |
| GCA<br>Ala<br>160 | TTT<br>Phe | GAA<br>Glu        | GAT<br>Asp        | GAA<br>Glu        | ATG<br>Met        | AAA<br>Lys<br>165 | AAG<br>Lys        | CTT<br>Leu        | CTC<br>Leu        | CTC<br>Leu        | TTC<br>Phe<br>170 | CTT<br>Leu        | AAA<br>Lys        | GCA<br>Ala | TTT<br>Phe        | 529  |
| TCT<br>Ser<br>175 | GAA<br>Glu | GCA<br>Ala        | GAG<br>Glu        | CAG<br>Gln        | ACA<br>Thr<br>180 | AAG<br>Lys        | TTG<br>Leu        | GCA<br>Ala        | ATG<br>Met        | CTG<br>Leu<br>185 | TCT<br>Ser        | GGG<br>Gly        | ATC<br>Ile        | CTG<br>Leu | TTG<br>Leu<br>190 | 577  |
| GGC<br>Gly        | AAT<br>Asn | GGA<br>Gly        | ACC<br>Thr<br>195 | CTC<br>Leu        | CCG<br>Pro        | GCC<br>Ala        | ACC<br>Thr        | ATC<br>Ile        | CTT<br>Leu<br>200 | ACC<br>Thr        | AGT<br>Ser        | CTC<br>Leu        | TTC<br>Phe<br>205 | ACC<br>Thr | GAC<br>Asp        | 625  |
| AGC<br>Ser        | TTA<br>Leu | GTC<br>Val        | AAA<br>Lys<br>210 | GAA<br>Glu        | GGC<br>Gly        | ATC<br>Ile        | GCA<br>Ala        | GCC<br>Ala<br>215 | TCG<br>Ser        | TTC<br>Phe        | GCT<br>Ala        | GTC<br>Val        | AAG<br>Lys<br>220 | CTT<br>Leu | TTC<br>Phe        | 673  |
| AAA<br>Lys        | GCC<br>Ala | TGG<br>Trp<br>225 | ATG<br>Met        | GCA<br>Ala        | GAG<br>Glu        | AAA<br>Lys        | GAT<br>Asp<br>230 | GCC<br>Ala        | AAT<br>Asn        | TCT<br>Ser        | GTC<br>Val        | ACC<br>Thr<br>235 | TCT<br>Ser        | TCA<br>Ser | TTG<br>Leu        | 721  |
| AGA<br>Arg<br>240 | AAA<br>Lys | GCC<br>Ala        | AAC<br>Asn        | CTG<br>Leu        | GAC<br>Asp        | AAG<br>Lys<br>245 | AGG<br>Arg        | CTG<br>Leu        | CTT<br>Leu        | GAA<br>Glu<br>250 | CTC<br>Leu        | TTC<br>Phe        | CCA<br>Pro        | GTG<br>Val | AAC<br>Asn        | 769  |
| AGA<br>Arg<br>255 | CAG<br>Gln | AGT<br>Ser        | GTG<br>Val        | GAT<br>Asp        | CAT<br>His<br>260 | TTC<br>Phe        | GCC<br>Ala        | AAG<br>Lys        | TAC<br>Tyr        | TTC<br>Phe<br>265 | ACT<br>Thr        | GAC<br>Asp        | GCA<br>Ala        | GGA<br>Gly | CTG<br>Leu<br>270 | 817  |
| AAG<br>Lys        | GAG<br>Glu | CTG<br>Leu        | TCA<br>Ser        | GAC<br>Asp<br>275 | TTT<br>Phe        | CTC<br>Leu        | CGA<br>Arg        | GTC<br>Val        | CAG<br>Gln<br>280 | CAG<br>Gln        | TCA<br>Ser        | CTG<br>Leu        | GGC<br>Gly<br>285 | ACC<br>Thr | AGG<br>Arg        | 865  |
| AAG<br>Lys        | GAA<br>Glu | CTG<br>Leu        | CAG<br>Gln<br>290 | AAG<br>Lys        | GAG<br>Glu        | CTG<br>Leu        | CAA<br>Gln<br>295 | GAG<br>Glu<br>295 | CGA<br>Arg        | CTG<br>Leu        | TCT<br>Ser        | CAG<br>Gln<br>300 | GAA<br>Glu<br>300 | TGC<br>Cys | CCC<br>Pro        | 913  |
| ATC<br>Ile        | AAG<br>Lys | GAG<br>Glu<br>305 | GTG<br>Val        | GTG<br>Val        | CTT<br>Leu        | TAC<br>Tyr<br>310 | GTC<br>Val<br>310 | AAA<br>Lys        | GAG<br>Glu        | GAA<br>Glu        | ATG<br>Met        | AAA<br>Lys<br>315 | AGG<br>Arg        | AAC<br>Asn | GAC<br>Asp        | 961  |
| CTT<br>Leu<br>320 | CCG<br>Pro | GAG<br>Glu        | ACA<br>Thr        | GCT<br>Ala        | GTG<br>Val<br>325 | ATC<br>Ile<br>325 | GGG<br>Gly        | CTG<br>Leu        | CTG<br>Leu        | TGG<br>Trp<br>330 | ACC<br>Thr<br>330 | TGC<br>Cys        | GTC<br>Val        | ATG<br>Met | AAC<br>Asn        | 1009 |
| GCT<br>Ala<br>335 | GTG<br>Val | GAA<br>Glu        | TGG<br>Trp        | AAC<br>Asn        | AAG<br>Lys<br>340 | AAG<br>Lys        | GAG<br>Glu        | GAG<br>Glu        | CTG<br>Leu        | GTT<br>Val<br>345 | GCT<br>Ala        | GAG<br>Glu        | CAG<br>Gln        | GCT<br>Ala | CTT<br>Leu<br>350 | 1057 |
| AAG<br>Lys        | CAC<br>His | CTG<br>Leu        | AAG<br>Lys        | CAA<br>Gln<br>355 | TAC<br>Tyr        | GCT<br>Ala        | CCC<br>Pro        | CTG<br>Leu        | CTG<br>Leu        | GCC<br>Ala<br>360 | GTG<br>Val        | TTC<br>Phe        | AGT<br>Ser        | TCC<br>Ser | CAA<br>Gln<br>365 | 1105 |
| GGC<br>Gly        | CAG<br>Gln | TCA<br>Ser        | GAG<br>Glu        | CTT<br>Leu        | GTC<br>Val        | CTC<br>Leu        | CTG<br>Leu        | CAG<br>Gln        | AAG<br>Lys        | GTT<br>Val        | CAG<br>Gln        | GAA<br>Glu        | TAC<br>Tyr        | TGC<br>Cys | TAT<br>Tyr        | 1153 |

| 370 |     |     |     |            |            |          |     |     |     | 375 |     |     |     |     | 380 |      |  |  |  |  |
|-----|-----|-----|-----|------------|------------|----------|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|--|--|--|
| GAC | AAC | ATC | CAC | TTC        | ATG        | AAA      | GCC | TTC | CAG | AAG | ATC | GTG | GTT | CTC | TTT | 1201 |  |  |  |  |
| Asp | Asn | Ile | His | Phe        | Met        | Lys      | Ala | Phe | Gln | Lys | Ile | Val | Val | Leu | Phe |      |  |  |  |  |
|     | 385 |     |     |            |            |          | 390 |     |     |     |     | 395 |     |     |     |      |  |  |  |  |
| TAT | AAA | GCC | GAC | GTT        | CTG        | AGC      | GAG | GAG | GCG | ATA | CTG | AAG | TGG | TAT | AAA | 1249 |  |  |  |  |
| Tyr | Lys | Ala | Asp | Val        | Leu        | Ser      | Glu | Glu | Ala | Ile | Leu | Lys | Trp | Tyr | Lys |      |  |  |  |  |
|     | 400 |     |     |            |            | 405      |     |     |     |     | 410 |     |     |     |     |      |  |  |  |  |
| GAA | GCA | CAT | GCC | GCC        | AAA        | GGC      | AAA | AGC | GTC | TTC | CTT | GAC | CAG | ATG | AAG | 1297 |  |  |  |  |
| Glu | Ala | His | Ala | Ala        | Lys        | Gly      | Lys | Ser | Val | Phe | Leu | Asp | Gln | Met | Lys |      |  |  |  |  |
|     | 415 |     |     |            | 420        |          |     |     |     | 425 |     |     |     |     | 430 |      |  |  |  |  |
| AAA | TTT | GTG | GAG | TGG        | TTA        | CAA      | AAT | GCA | GAA | GAA | GAA | TCT | GAA | TCA | GAA | 1345 |  |  |  |  |
| Lys | Phe | Val | Glu | Trp        | Leu        | Gln      | Asn | Ala | Glu | Glu | Glu | Ser | Glu | Ser | Glu |      |  |  |  |  |
|     |     |     |     | 435        |            |          |     |     | 440 |     |     |     |     | 445 |     |      |  |  |  |  |
| GGT | GAA | GAA | AGC | TAAATGTCTC | CAGCACACTG | CCTAAAAA |     |     |     |     |     |     |     |     |     | 1385 |  |  |  |  |
| Gly | Glu | Glu | Ser |            |            |          |     |     |     |     |     |     |     |     |     |      |  |  |  |  |
|     |     |     | 450 |            |            |          |     |     |     |     |     |     |     |     |     |      |  |  |  |  |

## (2) INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 450 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Pro | Gln | Pro | Leu | Pro | Pro | Pro | Leu | Leu | Leu | Gln | Asp | Pro | Pro | Gln |
| 1   |     |     |     | 5   |     |     |     | 10  |     |     |     |     |     | 15  |     |
| Pro | Pro | Val | Ser | Arg | Val | Val | Ala | Pro | Ser | Leu | Asp | Ser | Asn | Phe | Met |
|     |     | 20  |     |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Asn | Lys | His | Gln | Lys | Pro | Val | Leu | Thr | Gly | Gln | Arg | Phe | Lys | Thr | Arg |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Lys | Arg | Asp | Glu | Lys | Glu | Lys | Phe | Glu | Pro | Thr | Val | Phe | Arg | Asp | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Val | Gln | Gly | Leu | Asn | Glu | Ala | Gly | Asp | Asp | Leu | Glu | Ala | Val | Ala |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |
| Lys | Phe | Leu | Asp | Ser | Thr | Gly | Ser | Arg | Leu | Asp | Tyr | Arg | Arg | Tyr | Ala |
|     |     |     | 85  |     |     |     |     |     | 90  |     |     |     |     | 95  |     |
| Asp | Thr | Leu | Phe | Asp | Ile | Leu | Val | Ala | Gly | Ser | Met | Leu | Ala | Pro | Gly |
|     |     | 100 |     |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Gly | Thr | Arg | Ile | Asp | Asp | Gly | Asp | Lys | Thr | Lys | Met | Thr | Asn | His | Cys |
|     | 115 |     |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |
| Val | Phe | Ser | Ala | Asn | Glu | Asp | His | Glu | Thr | Ile | Arg | Asn | Tyr | Ala | Gln |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |
| Val | Phe | Asn | Lys | Leu | Ile | Arg | Arg | Tyr | Lys | Tyr | Leu | Glu | Lys | Ala | Phe |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |

Glu Asp Glu Met Lys Lys Leu Leu Leu Phe Leu Lys Ala Phe Ser Glu  
 165 170 175  
 Ala Glu Gln Thr Lys Leu Ala Met Leu Ser Gly Ile Leu Leu Gly Asn  
 180 185 190  
 Gly Thr Leu Pro Ala Thr Ile Leu Thr Ser Leu Phe Thr Asp Ser Leu  
 195 200 205  
 Val Lys Glu Gly Ile Ala Ala Ser Phe Ala Val Lys Leu Phe Lys Ala  
 210 215 220  
 Trp Met Ala Glu Lys Asp Ala Asn Ser Val Thr Ser Ser Leu Arg Lys  
 225 230 235 240  
 Ala Asn Leu Asp Lys Arg Leu Leu Glu Leu Phe Pro Val Asn Arg Gln  
 245 250 255  
 Ser Val Asp His Phe Ala Lys Tyr Phe Thr Asp Ala Gly Leu Lys Glu  
 260 265 270  
 Leu Ser Asp Phe Leu Arg Val Gln Gln Ser Leu Gly Thr Arg Lys Glu  
 275 280 285  
 Leu Gln Lys Glu Leu Gln Glu Arg Leu Ser Gln Glu Cys Pro Ile Lys  
 290 295 300  
 Glu Val Val Leu Tyr Val Lys Glu Glu Met Lys Arg Asn Asp Leu Pro  
 305 310 315 320  
 Glu Thr Ala Val Ile Gly Leu Leu Trp Thr Cys Val Met Asn Ala Val  
 325 330 335  
 Glu Trp Asn Lys Lys Glu Glu Leu Val Ala Glu Gln Ala Leu Lys His  
 340 345 350  
 Leu Lys Gln Tyr Ala Pro Leu Leu Ala Val Phe Ser Ser Gln Gly Gln  
 355 360 365  
 Ser Glu Leu Val Leu Leu Gln Lys Val Gln Glu Tyr Cys Tyr Asp Asn  
 370 375 380  
 Ile His Phe Met Lys Ala Phe Gln Lys Ile Val Val Leu Phe Tyr Lys  
 385 390 395 400  
 Ala Asp Val Leu Ser Glu Glu Ala Ile Leu Lys Trp Tyr Lys Glu Ala  
 405 410 415  
 His Ala Ala Lys Gly Lys Ser Val Phe Leu Asp Gln Met Lys Lys Phe  
 420 425 430  
 Val Glu Trp Leu Gln Asn Ala Glu Glu Glu Ser Glu Ser Glu Gly Glu  
 435 440 445  
 Glu Ser  
 450

## (2) INFORMATION FOR SEQ ID NO:85:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1463 base pairs  
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: HW094

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 255..1238

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: 1050..1355  
(D) OTHER INFORMATION: /label= SAC\_23896

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GTCGACCCCG AACACCCACA CTCGGTCCCC AGCCGTTTTT CTCCCAGAGA TCCGGAAGCC | 60  |
| CCGACGTCGT GCCCTACACC AAAGATCGAG AAAACCACTC AGACGCGGCT CCTAGGCGGC | 120 |
| AGTTCGGTTC CCATAGCAAC CCTCGGAGCA CCCGCATCCC GCTTCGGGCC GGGTGGCTCG | 180 |
| GGCGCTCCCG TGACGTCACG GCGCCGCTTT CCGGTGACTG AGTCGAGCTG AGGTTGTTGT | 240 |
| GGGCCGGGGG CGCC ATG GGG GCG ACT GGC GAC ACC GAG CAG CCG CGG GGC   | 290 |
| Met Gly Ala Thr Gly Asp Thr Glu Gln Pro Arg Gly                   |     |
| 1 5 10                                                            |     |
| CCC GGC GGG GCG GAG CGA GGC GGC CTG GAG CTG GGC GAC GCG GGC GCG   | 338 |
| Pro Gly Gly Ala Glu Arg Gly Gly Leu Glu Leu Gly Asp Ala Gly Ala   |     |
| 15 20 25                                                          |     |
| GCG GGC CAG CCG GTT CTC ACG AAC CCT TGG AAC ATA ATG ATC AAA CAC   | 386 |
| Ala Gly Gln Pro Val Leu Thr Asn Pro Trp Asn Ile Met Ile Lys His   |     |
| 30 35 40                                                          |     |
| CGG CAG GTG CAG CGA AGA GGC CGC CGA TCT CAG ATG ACC ACA AGT TTC   | 434 |
| Arg Gln Val Gln Arg Arg Gly Arg Arg Ser Gln Met Thr Thr Ser Phe   |     |
| 45 50 55 60                                                       |     |
| ACA GAT CCA GCC ATC TCT ATG GAT CTC CTC CGT GCT GTC CTG CAG CCT   | 482 |
| Thr Asp Pro Ala Ile Ser Met Asp Leu Leu Arg Ala Val Leu Gln Pro   |     |
| 65 70 75                                                          |     |
| AGC ATC AAT GAG GAG ATC CAG AGT GTC TTC AAC AAG TAC ATG AAG TTC   | 530 |
| Ser Ile Asn Glu Glu Ile Gln Ser Val Phe Asn Lys Tyr Met Lys Phe   |     |
| 80 85 90                                                          |     |
| TTC CAG AAG GCA GCG CTG AAT GTG CGA GAC AAC GTT GGT GAA GAG GTG   | 578 |
| Phe Gln Lys Ala Ala Leu Asn Val Arg Asp Asn Val Gly Glu Glu Val   |     |
| 95 100 105                                                        |     |
| GAT GCA GAA CAG TTG ATT CAG GAG GCC TGC CGC AGC TGC CTG GAG CAG   | 626 |
| Asp Ala Glu Gln Leu Ile Gln Glu Ala Cys Arg Ser Cys Leu Glu Gln   |     |
| 110 115 120                                                       |     |

|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| GCA AAG CTA CTC TTT TCA GAT GGA GAA AAA GTG ATA CCC AGA TTG GCC<br>Ala Lys Leu Leu Phe Ser Asp Gly Glu Lys Val Ile Pro Arg Leu Ala<br>125 130 135 140 | 674  |
| CAT GAA CTT CCA GGG ATC AAG CGT GGC CGG CAG GCA GAA GAG GAG TCC<br>His Glu Leu Pro Gly Ile Lys Arg Gly Arg Gln Ala Glu Glu Glu Ser<br>145 150 155     | 722  |
| CAC CGA GGA AGC CCC ATT CCC AAA AAG AGG AAA GGT CGG CCT CCT GGA<br>His Arg Gly Ser Pro Ile Pro Lys Lys Arg Lys Gly Arg Pro Pro Gly<br>160 165 170     | 770  |
| CAT GTC CTG TCA AAT GAC CGC GCA GCT GCT GGC ATG GTA TGG AAA CCA<br>His Val Leu Ser Asn Asp Arg Ala Ala Ala Gly Met Val Trp Lys Pro<br>175 180 185     | 818  |
| AAA TCC TGT GAA CCA ATT CGC CGA GAA GGC CCC AAG TGG GAC CCA GCT<br>Lys Ser Cys Glu Pro Ile Arg Arg Glu Gly Pro Lys Trp Asp Pro Ala<br>190 195 200     | 866  |
| CGG CTG AAT GAA TCT ACC ACC TTT GTT TTG GGG TCT CGA GCC AAC AAG<br>Arg Leu Asn Glu Ser Thr Thr Phe Val Leu Gly Ser Arg Ala Asn Lys<br>205 210 215 220 | 914  |
| GCC TTA GGG ATG GGA GGC ACC AGA GGG AGG ATT TAC ATC AAG CAC CCA<br>Ala Leu Gly Met Gly Gly Thr Arg Gly Arg Ile Tyr Ile Lys His Pro<br>225 230 235     | 962  |
| CAC CTC TTT AAG TAT GCA GCA GAT CCT CAG GAC AAG CAC TGG CTG GCT<br>His Leu Phe Lys Tyr Ala Ala Asp Pro Gln Asp Lys His Trp Leu Ala<br>240 245 250     | 1010 |
| GAG CAG CAT CAT ATG CGG GCA ACA GGA GGA AAG ATG GCG TAC CTT CTC<br>Glu Gln His His Met Arg Ala Thr Gly Gly Lys Met Ala Tyr Leu Leu<br>255 260 265     | 1058 |
| ATT GAG GAA GAC ATC CGA GAC TTG GCT GCC AGC GAT GAC TAC AGA GGA<br>Ile Glu Glu Asp Ile Arg Asp Leu Ala Ala Ser Asp Asp Tyr Arg Gly<br>270 275 280     | 1106 |
| TGC TTG GAC CTG AAG TTG GAG GAG CTG AAG TCC TTT GTT TTG CCA TCC<br>Cys Leu Asp Leu Lys Leu Glu Glu Leu Lys Ser Phe Val Leu Pro Ser<br>285 290 295 300 | 1154 |
| TGG ATG GTT GAG AAG ATG CGG AAA TAC ATG GAG ACA CTA CGG ACA GAA<br>Trp Met Val Glu Lys Met Arg Lys Tyr Met Glu Thr Leu Arg Thr Glu<br>305 310 315     | 1202 |
| AAT GAG CAT CGT GCT GCT GAA GCA ACT CCC CAG ACC TGAGCCGAGT<br>Asn Glu His Arg Ala Ala Glu Ala Thr Pro Gln Thr<br>320 325                              | 1248 |
| GTCCTGGCTA CTACACTTGG CAGTCTGCCT CCCAGACCCT CTTTCCCCGC CCGGCTGAGG                                                                                     | 1308 |
| CCATCATGGG GATGCGGTCT AGTTGGCTCT TAGCAGCATC AAGCTGTACA TGAGCTAGTT                                                                                     | 1368 |
| TGTAGTGACT CACTGCAGAG CCCCCAGAC TGGCTTGTGG TTCTGTTTCT AAAGTTATTG                                                                                      | 1428 |
| GAATAAGAAG CAATTAAACA AGTTTGTAAT AAAAA                                                                                                                | 1463 |

(2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```

Met Gly Ala Thr Gly Asp Thr Glu Gln Pro Arg Gly Pro Gly Gly Ala
 1 5 10 15
Glu Arg Gly Gly Leu Glu Leu Gly Asp Ala Gly Ala Ala Gly Gln Pro
 20 25 30
Val Leu Thr Asn Pro Trp Asn Ile Met Ile Lys His Arg Gln Val Gln
 35 40 45
Arg Arg Gly Arg Arg Ser Gln Met Thr Thr Ser Phe Thr Asp Pro Ala
 50 55 60
Ile Ser Met Asp Leu Leu Arg Ala Val Leu Gln Pro Ser Ile Asn Glu
 65 70 75 80
Glu Ile Gln Ser Val Phe Asn Lys Tyr Met Lys Phe Phe Gln Lys Ala
 85 90 95
Ala Leu Asn Val Arg Asp Asn Val Gly Glu Glu Val Asp Ala Glu Gln
 100 105 110
Leu Ile Gln Glu Ala Cys Arg Ser Cys Leu Glu Gln Ala Lys Leu Leu
 115 120 125
Phe Ser Asp Gly Glu Lys Val Ile Pro Arg Leu Ala His Glu Leu Pro
 130 135 140
Gly Ile Lys Arg Gly Arg Gln Ala Glu Glu Glu Ser His Arg Gly Ser
 145 150 155 160
Pro Ile Pro Lys Lys Arg Lys Gly Arg Pro Pro Gly His Val Leu Ser
 165 170 175
Asn Asp Arg Ala Ala Ala Gly Met Val Trp Lys Pro Lys Ser Cys Glu
 180 185 190
Pro Ile Arg Arg Glu Gly Pro Lys Trp Asp Pro Ala Arg Leu Asn Glu
 195 200 205
Ser Thr Thr Phe Val Leu Gly Ser Arg Ala Asn Lys Ala Leu Gly Met
 210 215 220
Gly Gly Thr Arg Gly Arg Ile Tyr Ile Lys His Pro His Leu Phe Lys
 225 230 235 240
Tyr Ala Ala Asp Pro Gln Asp Lys His Trp Leu Ala Glu Gln His His
 245 250 255
Met Arg Ala Thr Gly Gly Lys Met Ala Tyr Leu Leu Ile Glu Glu Asp
 260 265 270
Ile Arg Asp Leu Ala Ala Ser Asp Asp Tyr Arg Gly Cys Leu Asp Leu
 275 280 285

```



Lys Leu Glu Glu Leu Lys Ser Phe Val Leu Pro Ser Trp Met Val Glu  
290 295 300

Lys Met Arg Lys Tyr Met Glu Thr Leu Arg Thr Glu Asn Glu His Arg  
305 310 315 320

Ala Ala Glu Ala Thr Pro Gln Thr  
325

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1276 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: HW095

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 7..876

(ix) FEATURE:  
 (A) NAME/KEY: misc\_feature  
 (B) LOCATION: complement (631..798)  
 (D) OTHER INFORMATION: /label= SAC\_23802

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

|                                                                                                                                                   |     |
|---------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| GTTCGAC ATT TTC TCA GAA TCC TAC GGA GGA AAG ATG GCT GCT GGC ATC<br>Ile Phe Ser Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile<br>1 5 10              | 48  |
| AGT TTA GAA CTT CAC AAG GCT ATT CAG CAA GGG ACC ATC AAG TGC AAC<br>Ser Leu Glu Leu His Lys Ala Ile Gln Gln Gly Thr Ile Lys Cys Asn<br>15 20 25 30 | 96  |
| TTC TCT GGG GTT GCT TTG GGT GAC TCC TGG ATC TCC CCT GTG GAT TCA<br>Phe Ser Gly Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser<br>35 40 45    | 144 |
| GTG CTG TCC TGG GGA CCT TAC CTG TAC AGC GTG TCT CTC CTT GAT AAT<br>Val Leu Ser Trp Gly Pro Tyr Leu Tyr Ser Val Ser Leu Leu Asp Asn<br>50 55 60    | 192 |
| AAA GGC TTG GCT GAG GTG TCC GAC ATT GCG GAG CAA GTC CTC AAT GCT<br>Lys Gly Leu Ala Glu Val Ser Asp Ile Ala Glu Gln Val Leu Asn Ala<br>65 70 75    | 240 |
| GTA AAC AAG GGC TTC TAC AAG GAA GCC ACT CAG CTG TGG GGG AAA GCA<br>Val Asn Lys Gly Phe Tyr Lys Glu Ala Thr Gln Leu Trp Gly Lys Ala<br>80 85 90    | 288 |
| GAA ATG ATC ATT GAA AAG AAC ACC GAC GGG GTA AAC TTC TAT AAC ATC<br>Glu Met Ile Ile Glu Lys Asn Thr Asp Gly Val Asn Phe Tyr Asn Ile                | 336 |

| 95                                                                                                                                                    | 100 | 105 | 110 |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|-----|-----|------|
| TTA ACT AAA AGC ACC CCC GAC ACC TCT ATG GAG TCG AGC CTC GAG TTC<br>Leu Thr Lys Ser Thr Pro Asp Thr Ser Met Glu Ser Ser Leu Glu Phe<br>115 120 125     |     |     |     | 384  |
| TTC CGG AGC CCC TTA GTT CGT CTC TGT CAG CGC CAC GTG AGA CAC CTA<br>Phe Arg Ser Pro Leu Val Arg Leu Cys Gln Arg His Val Arg His Leu<br>130 135 140     |     |     |     | 432  |
| CAA GGA GAC GCC TTA AGT CAG CTC ATG AAC GGT CCC ATC AAA AAG AAG<br>Gln Gly Asp Ala Leu Ser Gln Leu Met Asn Gly Pro Ile Lys Lys Lys<br>145 150 155     |     |     |     | 480  |
| CTC AAA ATT ATC CCT GAC GAT GTC TCC TGG GGA GCC CAG TCA TCC TCC<br>Leu Lys Ile Ile Pro Asp Asp Val Ser Trp Gly Ala Gln Ser Ser Ser<br>160 165 170     |     |     |     | 528  |
| GTC TTC ATA AGC ATG GAA GAG GAC TTC ATG AAG CCT GTC ATC GAC ATC<br>Val Phe Ile Ser Met Glu Glu Asp Phe Met Lys Pro Val Ile Asp Ile<br>175 180 185 190 |     |     |     | 576  |
| GTG GAT ACG TTG CTG GAA CTC GGG GTC AAT GTG ACT GTG TAC AAT GGG<br>Val Asp Thr Leu Leu Glu Leu Gly Val Asn Val Thr Val Tyr Asn Gly<br>195 200 205     |     |     |     | 624  |
| CAG CTG GAT CTC ATT GTG GAC ACC ATA GGT CAG GAG TCC TGG GTT CAG<br>Gln Leu Asp Leu Ile Val Asp Thr Ile Gly Gln Glu Ser Trp Val Gln<br>210 215 220     |     |     |     | 672  |
| AAG CTG AAG TGG CCA CAG CTG TCC AGA TTC AAT CAG CTA AAA TGG AAG<br>Lys Leu Lys Trp Pro Gln Leu Ser Arg Phe Asn Gln Leu Lys Trp Lys<br>225 230 235     |     |     |     | 720  |
| GCC CTG TAC ACC AAT CCT AAG TCT TCA GAA ACA TCT GCG TTT GTC AAG<br>Ala Leu Tyr Thr Asn Pro Lys Ser Ser Glu Thr Ser Ala Phe Val Lys<br>240 245 250     |     |     |     | 768  |
| TCC TAT GAG AAC CTA GCG TTC TAC TGG ATC CTA AAG GCG GGT CAC ATG<br>Ser Tyr Glu Asn Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met<br>255 260 265 270 |     |     |     | 816  |
| GTT CCT GCT GAC CAA GGG GAC ATG GCT CTG AAG ATG ATG AGG CTG GTT<br>Val Pro Ala Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val<br>275 280 285     |     |     |     | 864  |
| ACT CAG CAG GAG TAGCTGAGCT GAGCTGGCCC TGGAGGCCCT GGAGGCCCTG<br>Thr Gln Gln Glu<br>290                                                                 |     |     |     | 916  |
| GAGGCCCTGG AGTAGGGCCC AGGATGCAGG TGCTAATGTC TATCCCCGGC GCTCTTCTTC                                                                                     |     |     |     | 976  |
| CCGACTCTAC CATGGGATGT AACTCCAGGA GCCCCTGCCA TCTCCGGTAC CAAAAGACTG                                                                                     |     |     |     | 1036 |
| TGGCTTCCGT GTCTACTCAG AAATCAGTTC TACTTCGTAA ACAGTGTTTA AAACCAGACT                                                                                     |     |     |     | 1096 |
| CATTTAATCA GAGTGAAGGA TTGCAGTCCA TTGGCTTCTT AGCACAGAAG CAGCTGATAA                                                                                     |     |     |     | 1156 |
| CACAAGTAAA CCCCAGCCCT TGAGAGGTAG AAGCAAGAGG ATCAGAGGTT CAAGCGCATC                                                                                     |     |     |     | 1216 |
| CTCGGCTCCA TCACAAGTTC AAAAGCCGCC TGCACCAAAT GGGAGTCCTT GTCTCAAAAA                                                                                     |     |     |     | 1276 |

## (2) INFORMATION FOR SEQ ID NO:88:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

Ile Phe Ser Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Ser Leu
 1 5 10 15
Glu Leu His Lys Ala Ile Gln Gln Gly Thr Ile Lys Cys Asn Phe Ser
 20 25 30
Gly Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu
 35 40 45
Ser Trp Gly Pro Tyr Leu Tyr Ser Val Ser Leu Leu Asp Asn Lys Gly
 50 55 60
Leu Ala Glu Val Ser Asp Ile Ala Glu Gln Val Leu Asn Ala Val Asn
 65 70 75 80
Lys Gly Phe Tyr Lys Glu Ala Thr Gln Leu Trp Gly Lys Ala Glu Met
 85 90 95
Ile Ile Glu Lys Asn Thr Asp Gly Val Asn Phe Tyr Asn Ile Leu Thr
 100 105 110
Lys Ser Thr Pro Asp Thr Ser Met Glu Ser Ser Leu Glu Phe Phe Arg
 115 120 125
Ser Pro Leu Val Arg Leu Cys Gln Arg His Val Arg His Leu Gln Gly
 130 135 140
Asp Ala Leu Ser Gln Leu Met Asn Gly Pro Ile Lys Lys Lys Leu Lys
 145 150 155 160
Ile Ile Pro Asp Asp Val Ser Trp Gly Ala Gln Ser Ser Ser Val Phe
 165 170 175
Ile Ser Met Glu Glu Asp Phe Met Lys Pro Val Ile Asp Ile Val Asp
 180 185 190
Thr Leu Leu Glu Leu Gly Val Asn Val Thr Val Tyr Asn Gly Gln Leu
 195 200 205
Asp Leu Ile Val Asp Thr Ile Gly Gln Glu Ser Trp Val Gln Lys Leu
 210 215 220
Lys Trp Pro Gln Leu Ser Arg Phe Asn Gln Leu Lys Trp Lys Ala Leu
 225 230 235 240
Tyr Thr Asn Pro Lys Ser Ser Glu Thr Ser Ala Phe Val Lys Ser Tyr
 245 250 255
Glu Asn Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro
 260 265 270

```

Ala Asp Gln Gly Asp Met Ala Leu Lys Met Met Arg Leu Val Thr Gln  
 275 280 285

Gln Glu  
 290

(2) INFORMATION FOR SEQ ID NO:89:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 2421 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: HW096

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 295..1302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

|                                                                   |          |
|-------------------------------------------------------------------|----------|
| GTCGACGTCT GATTTTACAT TCATGCAGTT GGGAGTAAGA GGAAAAAGAT TCTGAAGTGT | 60       |
| GGGGAAC TTC ACAAGAGGG GAACAAAGTC TGTGTCTATG GCTCCAAGGG AGAGAACATC | 120      |
| AGAGACACTC TGAGGAAGGA CGGCAGGTTT TGTTCTTTCA TAGAGAATAA CCATTGGAAA | 180      |
| CTCATTAATG ACCTGGACAC TATCATAGAA AACACTCAGC CATTTGATGA GTTGGAGGGC | 240      |
| AAGCTCTTTC AGGTTGCAGC TGAGCTACCA AAGAACCCTA GGGTAGTCTC TGTC ATG   | 297      |
|                                                                   | Met<br>1 |
| CAG AAT TCT GGG TTA GAG AAC AGA GAC TTC CAT AAG CTA GAA GAC TAT   | 345      |
| Gln Asn Ser Gly Leu Glu Asn Arg Asp Phe His Lys Leu Glu Asp Tyr   |          |
| 5 10 15                                                           |          |
| ATT GTG AAT GCG AAC CCT ACA TTG AAA GAA GAA GGA GAA AAA CTC AGA   | 393      |
| Ile Val Asn Ala Asn Pro Thr Leu Lys Glu Glu Gly Glu Lys Leu Arg   |          |
| 20 25 30                                                          |          |
| GCA TAC ATC AAG AAA GAA AGT AAA AAA AGA AAG AAA GGT TCC TTA TTC   | 441      |
| Ala Tyr Ile Lys Lys Glu Ser Lys Lys Arg Lys Lys Gly Ser Leu Phe   |          |
| 35 40 45                                                          |          |
| AAA GTG CAT AAA GAA CAC TTT GGG AAA ATA ACA AAA AAT TCT ACT CCT   | 489      |
| Lys Val His Lys Glu His Phe Gly Lys Ile Thr Lys Asn Ser Thr Pro   |          |
| 50 55 60 65                                                       |          |
| GTT AAA GTG CAC AAA CAT CTT TCG AAA GTC AGT GAT TCA GTT GGG TTC   | 537      |
| Val Lys Val His Lys His Leu Ser Lys Val Ser Asp Ser Val Gly Phe   |          |
| 70 75 80                                                          |          |
| CTA TGG TGG AAC AAC AAT GGA AAG GAG GGC TGT GCC ACC TGC TTT GTT   | 585      |
| Leu Trp Trp Asn Asn Asn Gly Lys Glu Gly Cys Ala Thr Cys Phe Val   |          |

| 85                                                                |     |     |     |     |     |     | 90  |     |     |     |     | 95  |     |     |     |      |  |
|-------------------------------------------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| TTT                                                               | AAA | GGA | TTA | TAC | ATT | TTG | ACT | TGC | CGG | CAT | GTG | ATA | ACT | AGT | ATT | 633  |  |
| Phe                                                               | Lys | Gly | Leu | Tyr | Ile | Leu | Thr | Cys | Arg | His | Val | Ile | Thr | Ser | Ile |      |  |
| 100                                                               |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| GTG                                                               | GGT | GAA | GGC | ATA | GAT | CCA | TGT | CAG | TGG | GCA | AGC | TTA | ATT | AGT | CAG | 681  |  |
| Val                                                               | Gly | Glu | Gly | Ile | Asp | Pro | Cys | Gln | Trp | Ala | Ser | Leu | Ile | Ser | Gln |      |  |
| 115                                                               |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| TGT                                                               | GTA | AAG | GTG | ACC | TTT | GGT | TAT | GAA | GAG | TTC | CCA | CTA | GTA | GAA | GAC | 729  |  |
| Cys                                                               | Val | Lys | Val | Thr | Phe | Gly | Tyr | Glu | Glu | Phe | Pro | Leu | Val | Glu | Asp |      |  |
| 130                                                               |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| AAG                                                               | TTT | TTT | GAG | GTT | AAA | CCT | TGG | TTT | GAG | ATA | TCT | AAT | GAA | AGC | CTT | 777  |  |
| Lys                                                               | Phe | Phe | Glu | Val | Lys | Pro | Trp | Phe | Glu | Ile | Ser | Asn | Glu | Ser | Leu |      |  |
| 150                                                               |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| GAC                                                               | TAT | GCT | GTC | CTA | GAA | CTG | AGG | GAA | AAT | GGA | CAA | GAA | GTT | CCT | GCT | 825  |  |
| Asp                                                               | Tyr | Ala | Val | Leu | Glu | Leu | Arg | Glu | Asn | Gly | Gln | Glu | Val | Pro | Ala |      |  |
| 165                                                               |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| GGA                                                               | CTG | TAT | AAT | GGA | ATA | GGA | CCT | GTG | CCA | CTT | GGT | GGG | TTA | ATA | TAT | 873  |  |
| Gly                                                               | Leu | Tyr | Asn | Gly | Ile | Gly | Pro | Val | Pro | Leu | Gly | Gly | Leu | Ile | Tyr |      |  |
| 180                                                               |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| ATC                                                               | ATT | GGC | CAT | CCT | GAT | GGA | GAA | AAG | AAG | TCT | ACT | GAT | GGC | TGT | GCA | 921  |  |
| Ile                                                               | Ile | Gly | His | Pro | Asp | Gly | Glu | Lys | Lys | Ser | Thr | Asp | Gly | Cys | Ala |      |  |
| 195                                                               |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| GTG                                                               | GTC | CCT | CAA | AGT | CAT | AGA | GGG | CAA | AAA | TGT | CAG | GAA | AAT | TTT | CAA | 969  |  |
| Val                                                               | Val | Pro | Gln | Ser | His | Arg | Gly | Gln | Lys | Cys | Gln | Glu | Asn | Phe | Gln |      |  |
| 210                                                               |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| GCA                                                               | AGA | GAG | AAA | GCA | AAC | TAC | TGG | ATT | TCT | ACA | TCT | TTT | TTT | CCT | ATA | 1017 |  |
| Ala                                                               | Arg | Glu | Lys | Ala | Asn | Tyr | Trp | Ile | Ser | Thr | Ser | Phe | Phe | Pro | Ile |      |  |
| 230                                                               |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| TAC                                                               | ACA | CAA | AGA | AGT | TTC | CAC | GAA | GTC | TTT | CAC | AAC | CAT | GAT | GTG | GTT | 1065 |  |
| Tyr                                                               | Thr | Gln | Arg | Ser | Phe | His | Glu | Val | Phe | His | Asn | His | Asp | Val | Val |      |  |
| 245                                                               |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| ACT                                                               | TAT | GAC | ACC | ACT | TTT | TTT | GGT | GGG | TCT | TCT | GGA | TCC | CCA | GTA | TTT | 1113 |  |
| Thr                                                               | Tyr | Asp | Thr | Thr | Phe | Phe | Gly | Gly | Ser | Ser | Gly | Ser | Pro | Val | Phe |      |  |
| 260                                                               |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| GAT                                                               | TCT | AAT | GGT | TCA | TTG | GTG | GCC | ATG | CAT | GCT | GCT | GGC | ATC | ACT | TGT | 1161 |  |
| Asp                                                               | Ser | Asn | Gly | Ser | Leu | Val | Ala | Met | His | Ala | Ala | Gly | Ile | Thr | Cys |      |  |
| 275                                                               |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| ACA                                                               | GAC | CAG | AAT | GGA | GTT | TTT | AAT | ATC | ATT | GAG | TTT | GGT | TTT | ACT | ATG | 1209 |  |
| Thr                                                               | Asp | Gln | Asn | Gly | Val | Phe | Asn | Ile | Ile | Glu | Phe | Gly | Phe | Thr | Met |      |  |
| 290                                                               |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| GAA                                                               | TCC | ATT | CTT | GCT | AAT | ATT | AAG | CAA | ACT | AAA | GAG | TGG | TAT | GAT | ACC | 1257 |  |
| Glu                                                               | Ser | Ile | Leu | Ala | Asn | Ile | Lys | Gln | Thr | Lys | Glu | Trp | Tyr | Asp | Thr |      |  |
| 310                                                               |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| ATT                                                               | TTT | GTA | AAT | GAT | CGG | GAT | GCA | GAA | ATG | CTG | AGC | ACA | GAC | TCC |     | 1302 |  |
| Ile                                                               | Phe | Val | Asn | Asp | Arg | Asp | Ala | Glu | Met | Leu | Ser | Thr | Asp | Ser |     |      |  |
| 325                                                               |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| 330                                                               |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| 335                                                               |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| TGAGGACTGG AAAGGGTGTA TTCTAGTTCA CAACTTTAAG GGAATTGCCT AAGGTGTTTT |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |
| 1361                                                              |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |  |

|                                                                    |      |
|--------------------------------------------------------------------|------|
| TCTTCAGATA ATAATGTTTT ATGAACTTTC AAAATGATTA ATTTCACCCA ATAATCATAG  | 1422 |
| TTCTAGAGTG TATCTTAACT ATCAAGCATT TTCATGGTTT ATTAAAACAA ACAATCAAAA  | 1482 |
| ACAAAACATAT CAGTTGAACT ATTTGTGTAA AGTAGCATGA AAAAGAGGAT TAAGTGCTGA | 1542 |
| TGTGGGATCC GAGGGTCAGG AGATGCTAAG ATGTGAAAAA GTTGAGAGCA TAAACTGGAG  | 1602 |
| TTATTAGCCA GAAGATTCAT GGAAAAGAAA GAAGCCTACC ACGTTCCTTG AAACCTAAAC  | 1662 |
| CAATTTCAAA CTCACATCAT TGGTTCCTACC CATATCTTCC TTCTCTGCTG ACCAGAGCTC | 1722 |
| AGCCAGGACA CTGAATCACA GCGACTTAAC CCTCCCAGGG CCCTGAACAT GGTGGCATT   | 1782 |
| CTTCCATTTT GTCTTTTAA CTTAAGACTT AGATCTGAAA TGAACCCACA TGAAGTGGCA   | 1842 |
| TGGAAATCAT TGAGCAAGCA AGGAGCTGGT CTCTGCCACA GAATGCATGT ACCTGAGACT  | 1902 |
| TTCTGGACTT GAGTTGTGGA GAGCAAACAT TGGAATAGGT GGTTCCTACT TGATACGATT  | 1962 |
| CACAATGGAG AGTGCTAGGA GGATATTGGG CACAACCTAG GACAATTCTC AGCAGTGTGA  | 2022 |
| CACTCAAGTC TTGGTCCTTT GAAGAGAAAAG AAAACTGCGT TCAAGAAGTA ATCTCATCAA | 2082 |
| AAACAGAGTC AAGGAGAATT TATGAACAGA AGACCAGAGA TCTTAGATTA TTTGAGAGAA  | 2142 |
| AGTAGGAATA GATGAGATGC TGAAGGAATG TTGCTGGGAT CCAGCGATTG CTTCAATTCT  | 2202 |
| TCCTTTATCA TAACTGAAAT ATGTCCTGTA TGAGAGCTAA CATGATCCTA ATCCACAAC   | 2262 |
| CCCCTTATTT TCCAGACATT TCCTAGTGCT ATTGTGTGAT ATTTTGTGTC CCCTGCCCAA  | 2322 |
| TGTATTTTTC CCAATCAAA TACAGGTGAA TCAATTAAAA AACAGTGTA TATCTGTAGT    | 2382 |
| AGGTTTTGAA ATATAAGATG AAAAAATTAA AAAGTCGAC                         | 2421 |

## (2) INFORMATION FOR SEQ ID NO:90:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 336 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Gln | Asn | Ser | Gly | Leu | Glu | Asn | Arg | Asp | Phe | His | Lys | Leu | Glu | Asp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Tyr | Ile | Val | Asn | Ala | Asn | Pro | Thr | Leu | Lys | Glu | Glu | Gly | Glu | Lys | Leu |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Arg | Ala | Tyr | Ile | Lys | Lys | Glu | Ser | Lys | Lys | Arg | Lys | Lys | Gly | Ser | Leu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Phe | Lys | Val | His | Lys | Glu | His | Phe | Gly | Lys | Ile | Thr | Lys | Asn | Ser | Thr |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Pro | Val | Lys | Val | His | Lys | His | Leu | Ser | Lys | Val | Ser | Asp | Ser | Val | Gly |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |

**SUBSTITUTE SHEET (RULE 26)**

(vii) IMMEDIATE SOURCE:  
(B) CLONE: HW097

(ix) FEATURE:  
(A) NAME/KEY: misc\_feature  
(B) LOCATION: complement (203..553)  
(D) OTHER INFORMATION: /label= SAC\_23978

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GTGACTATT ACTATAGCCT TGTATATACT CCCCTCCGGC CCTGTTTGTC TCAGTCCCAT  | 60  |
| TCCCTCTTGT CTCTGAGAAT CATCCCCCAG CCCCAAGTTC TCCCTTCTGT CTCCCCCAC  | 120 |
| CCCCCTGCC TCCATTCTC CTGTCTCTGA ATGCCCTTGC CTGTATAAAG AGTTGGATTC   | 180 |
| TCCCTGGTG TCTGTACTGT GTACACACAT CCCTTTGAGA AGCACAAGGA GATGACACGC  | 240 |
| GCATTGTAAC CTTCACTCTG TCTCGGTGGC GACATAAAGG AAGCTGTGAA TTACAAGCTC | 300 |
| TGCCTCTTTC TGGCCTCTCC CTCGGCCCCC ATGACCGGGG CACTCTCTGC CCTCCCCACG | 360 |
| GCCTTAACAT GTTCCTGCTC CACCTATCCT GGTGCCCTTT GTCTGGCTGA CTGTAGCCTC | 420 |
| CCTGAGGGAA GGGATTGCTG GAGAGGTAGC TCCTATCCAG GAATGAAGGA CACTGGCTGG | 480 |
| AAACTAAGCC AAGAATGTTA CAGACAGGGG GAGCTGGGGA TTGGTGACTG ACCCTTGCAG | 540 |
| TTGGGCAGTG AGTACCCAAG GCCAGAAGCT GAAGCCCTCA TTCATTCACT GGCCTTTCTT | 600 |
| TCCTCAGGGT GCCCAGTGCC CTGTCCTCAC TTTGATGCCT AGGCCCACTG CTTGCATTTT | 660 |
| CTGGTGAGCC AGGGCTTGGT CATGTGAGGA AAGAGGTAGG CCTAGAGCAG GAGTTGAAAG | 720 |
| CCCTGCTGTT GTGTGTCCCT ACCATACAGG GCTGGCTAAA AGTCGAGGTA GACGCTTATC | 780 |
| TAGGAAGCGC AAGGCCCTGG GTTCGGTCCC CAGCTCGGAA AAAAAAGAAC CAAAAA     | 836 |

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 318 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: SAC23798

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

|                                                                   |    |
|-------------------------------------------------------------------|----|
| GGGGGATCCG CCCGATCCAA GACTGCCCAG GGTGGCTGCT CCATCTCACC CAGAGCAACC | 60 |
|-------------------------------------------------------------------|----|



|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGAGCTGGAC CTGGGGGTCG GAGCACTTCG AAGGTGATGG GTTATGGTGC CGCCTGCTGG | 120 |
| ACATAGTTGT CCAGAGCTCT TCCTGAAAGG TTTGCTACAG GATTCGCCCT TCTCATCCAG | 180 |
| TCTAAGAAAC TACTTAGTCA ACTCCTAGTG TCTAAGCAGA AGGCTTCAGC TATGGCTTCT | 240 |
| CCCCTTGGGG AGGAAGAGGA AGAGGTACAA ATTCTTGTTT TGCTGCTCCC AGGGAAAAGA | 300 |
| TCGGGCTAGA GCGGCCGC                                               | 318 |

## (2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 278 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: SAC\_23800

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGGGGATCCG CCCGATCACA CGGCTGCCTT CTGGTATACA GCAGAGGGGA ATGCCAAGGT | 60  |
| ATAAGTATCC TTCAATTCCT TCTTTGCCAC ATACCAGCAT TTCTTTGCCC TTTTGGCATT | 120 |
| CTACCTCTTC TTTGACAGCA CTGAGACTGT TAAGTGCTGC ATACAAGCTA CTTGTCTCCC | 180 |
| TATCTGTNNG CACATGTTTC ATGTCATGAA GATGATAAGG TCAGGCAAAG AGGCATGAAG | 240 |
| ATTCTGAAT AGTGCCCAAG TCGGGCTAGA GCGGCCGC                          | 278 |

## (2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 393 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: SAC\_23801

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGGGGATCCG CCCGATCCAG TAGCGACAGC CCTGGCCCTT GACGAGGATG GAAGTGACGT | 60  |
| TGTAGCNATT GTCTTCTGT AGCTCATAGA TGGTGCTGTN NATGGTAAAG CGGCTTTGTC  | 120 |

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| TTTCTTTCTG GACCGCATTG CCTGCCAGGN NGACAACGAA CCACCTGCCC TGGAACCGTT  | 180 |
| CGGTCCAGAA GCCTGGCTGC AGGGGCACAC TGATCGATCC AGTAGCGACA GCCCTGGCCC  | 240 |
| CTGACGAGGA TGGAAGTGAC GTTGTAGCTA TTGTCTTCCT GTAGCTCATA GATGGTGTCTG | 300 |
| TACATGGTAA AGCGGCTTTG TCTTTCTTTC TGGACCGCAT TGCCTGCCAG GCCGACAACG  | 360 |
| AACCACCTGC CCTGGAACCG TTCGGTCCAG AAG                               | 393 |

## (2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 531 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (vii) IMMEDIATE SOURCE:  
 (B) CLONE: SAC\_23833

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGGGGATCCG CCCGATCTGT ATCTCGTCCC TTGGCTGGCT GAGCCTCTGG AGGAGGTGTC | 60  |
| CAAAGCCCCG GTGGATTTCT GTCTCAGGGG TCTCTGTGAG ATTGAACTTG AGACCTTCTA | 120 |
| GAATCTCTTC CATGCTGTTG CCCTTTGCTC CCAGGGACAC GACGGCCAAG GCGGCTGAGA | 180 |
| TGCTAAGTGG GGAGAAGACA ACATTTTAT CTGGATTCCCT CAAAGCCAGC TTCCTGTAGA | 240 |
| GGCTGAAGGC AAAGTCAGTA TTGATGGAAG CCAGTGTGAG ACTGTCCAGT TGTGTCCCCT | 300 |
| TGTCTTGGTC TTCATGGAAT AGAGTGTCTT CTCCAGTAT GCAAATCTGG GAAGCAGAGG  | 360 |
| AGAGCAGAGC CCGATCGATC AAGATGACTA AGATGCTCAA AGGATTCGAC GCTGTGGGAA | 420 |
| ATGCCACAGG TTTCCGGTTC GCCTACACCC CAGCTATGGA GAGCCTCTGT GGATATGTCA | 480 |
| CAAGTCCAGA ACCGCAGCGA GGAGTTTCTC ATCGCGGGCC GTTTAAGGAC G          | 531 |

## (2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 274 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:

(B) CLONE: SAC\_23836

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGGGGATCCG CCCGATCATG ATGAATCCCC TGGGACCAAG CTATAACACA CAGTCCTCTG | 60  |
| AGAAAAAGGA TTGTGGTTTG CAGCAAATTC AGCCAATTTT GTCAAGCAAT TTGTGAGAGA | 120 |
| CACTCCTTAC TTGGTTGTTT CCTTCTCAGT CTTACGGGGT GCCTTATCAC TCCGTGATGG | 180 |
| TTCATGGCCA CACAGTCATA TTTCAGGGAG AAGTCCTTGT CGGTCACACC AGTTATCCTT | 240 |
| AACAGTGAGG TTAAGCAAAT CATGCCATTG CTGG                             | 274 |

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 254 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: SAC\_23853

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

|                                                                    |     |
|--------------------------------------------------------------------|-----|
| GGGGGATCCG CCCGATCGTG TTATTGAGGT CATCCACGGT GGAGATTAGC AGGTGACTCC  | 60  |
| GTTTTCTCTGG AAATGAGTGG AGTTGGGAAG GGGACCCGTG GCCGTGCTCC AGCTATAGTT | 120 |
| GGTGGGCGGT GGTTCGCTGC GAGCTTCACA GGTCAGGTTC ACGTTAGTAG GCCCAATGTA  | 180 |
| CCAGTTGCCT TCATAGCCAG AGATGGACAC TTCGGGTGGA TAAGGTAGGG AAAGGATCGG  | 240 |
| GCTAGAGCGG CCGC                                                    | 254 |

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: SAC\_23906

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GGGGGATCCG CCCACAGAAC CCAGAGGAAG GAGAGGCTGC TGGGGTGGAG GCCTAGGCGC 60  
TGGAGACATG TGGAGTTCTC TAGGGGTCTG CAGCAACCTC GGAAAGCTGG GAGATTCCCT 120  
CCTTGAGACT CCTACATATA GAAAACTGAT GCTTCTGTCT CATTCCATGC GGCTTTTCCT 180  
GCGGTATTCC TGTAGCGCTT TCTCTGCCAC TGTGTCCATA AACTTAGGGT TATCCTTGA 240  
GACTTCTTCT GGTAC 255

## (2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 219 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (vii) IMMEDIATE SOURCE:  
(B) CLONE: SAC\_23907

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GGGGGATCCG CCCACCCCAT CTAATCCTCT GAGGCTCAGG GTGACTCATT CTCCTTGA 60  
CCCAGGGGCG GGGCCGACAT TTGTTCCCCC AGTTGGGCC TGCTGCCCCA GGCCAGTGGC 120  
ATTCCAGTG TCTCCAGCCA CTAAAGCCAC ATTCTCAGG TAGTTGGTAT TGAAGCAGTT 180  
GGCTTGTTTA TCTCCAGGAG ACAAGGTTG AGCGGCCGC 219

## (2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (vii) IMMEDIATE SOURCE:  
(B) CLONE: SAC\_23916

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GGGGGATCCG CCCTCGAGCG GCCGCCACA AGAGATTGAA CCTAGAGCTG TGTGCCTCCT 60

GGGCAAGCAC TCTCTACTGA GCTACATCCC TGTTAAAGTG CCTTTTTTGG GAGCTTTGTC 120  
TTCCAGCCTG CCAATCAACC CACTTTATGG GTGTGCCTAG ATTCCCCTTT CTCTGAGTAG 180  
GG 182

(2) INFORMATION FOR SEQ ID NO:101:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 191 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: SAC\_23922

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGGGGATCCG CCCACTGTTC TCAAACAGTT GCCTAACAAT ACATTTAATT AAGAAATTAT 60  
CATAACTGTA TGCTTACACA TATGTGGATA GGCATCAATG AAGATTACAA CAGCTCAGCC 120  
ACAGTGCTGC AATGCTCTAC ACTACTACAA AACACCCACC ACGGGCCTGN NACCTGCCCT 180  
CGAGCGGCCG C 191

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 234 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
(B) CLONE: SAC\_24030

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GGGGGATCCG CCCACCATAT CTATACGGCC CTGGAAGAGG AGATAGAGCG AAACAAGCAG 60  
AACCAGTCT ATGCCCCGCT CTACTTNCCT GAGGAGCTGC ACCGAAGGCT GCCCTAGAGC 120  
AGGACATGGC CTTCTGGTAT GGGCCCCACT GGCAGGAGGC CATCCCTTAN NNACCAGCCA 180  
CACAGCACTA CGTAAAGCGT CTCCACGAGG TGGGAGGTGG GCTAGAGCGG CCGC 234

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 172 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
      (B) CLONE: SAC\_24078

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGGGGATCCG CCCGATCAAG ATGACTAAGA TGCTCAAAGG ATTCGACGCT GTGGGAAATG | 60  |
| CCACAGGTTT CCGGTTTCGCC TACACCCAG CCATGAGAGC CTCTGTGGAT ATGTCCACAA | 120 |
| GTCCCAGAAC CCGCAGCGAG GAGTTTCTCA TCGCGGGCCG TTTAAGGAAC GG         | 172 |

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 241 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
      (B) CLONE: SAC\_24105

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGGGGATCCG CCCGATCTGT GCATGTGAGC CGAACAGAAG TCAGCAATAA CCATGTCTTG | 60  |
| ATTTACCTGG ATAAGGTGTC AAATCAGACG GTGAACTTGT CCTTCACGGC TCAGCAAGAT | 120 |
| ATTCCAATAA GGGACCTGAA GCCAGCCGTA GTGAAAGTCT ACGATTACTA TGAGAAAGAT | 180 |
| GAGTTTGCAG TTGCAAATA CAGCGCTCCC TGCAGCACAG ATTATGGAAA TGCCTGAGGA  | 240 |
| C                                                                 | 241 |

(2) INFORMATION FOR SEQ ID NO:105:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 234 base pairs  
    (B) TYPE: nucleic acid  
    (C) STRANDEDNESS: double  
    (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(vii) IMMEDIATE SOURCE:  
(B) CLONE: SAC\_24140

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGGGGATCCG CCCGATCCTT AAAGGTCCCA TAACCAAGTA CTCCATGCAG TCATCTCCTC | 60  |
| TAACCTGTGG GTCCCTCCA TTCATTGCAA GCTGCTGGAC ATAGCCTGCT GGGTCCACCA  | 120 |
| CAAGTACAAC AGTGACAAGT CCAGCACCTA TGTGAAGAAT GGCACATCCT TCGACATCCA | 180 |
| CTACGGCTCA GGTAGCCTCT CTGGGTACCT GAGCCAGGAC ACTGTGTTGG TTCC       | 234 |

(2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 217 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(vii) IMMEDIATE SOURCE:  
(B) CLONE: SAC\_24142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGGGGATCCG CCCGATCTAT CCGGGTATAT TCGGAACGTG GGAGTCTGAC CGCAGTGCAC | 60  |
| TGCTACTCAG CTCACTCTGT CTCTTTCTCA CTGTGGGAGT AGCTATGGGA AAGGTCACAC | 120 |
| TTCTTGCTT TCCCTCAAA CCAACAGGGC TTCACTTCT CAGTCTCCCA ACGCACTGCA    | 180 |
| CACTGTCCC AGCATCCCGC ACAGTCTCAC CACACAC                           | 217 |

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 172 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(vii) IMMEDIATE SOURCE:  
(B) CLONE: SAC\_24192

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGGGGATCCG CCCACATCTC AGCGGTGGGG ACTCAGACAT TCCTGTGTTC CCTCCTTGGC | 60  |
| CTCCAGCCTC TCTGTAGGAA CCTCCAGCAG CCTGCCACCA GATTTCCTT AGCTTCCACT  | 120 |
| GTCTCCATGA GCTTTAAAT GTGGGCGGCC GCTCGAGGGC TAGAGCGGCC GC          | 172 |

## (2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 212 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: SAC\_24296

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGGGGATCCG CCCACTTGGC TGACCGCCAG GCGAGTGA CTGACTCCAG GTTCGCCCAC   | 60  |
| TACCGCAGCA GATACTGCCT CGCCTATGCC ACCTTCATAG TAGTGGTCCT CCACGGTGAG | 120 |
| GATCCTGCCT TTGGTTGCTC TGGCACAGTC GAGAATGAGC TTTTGTCCA GGGGCTTGAT  | 180 |
| GGTGAAGGGG TCCAGTGGGC TAGAGCGGCC GC                               | 212 |

## (2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 210 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(vii) IMMEDIATE SOURCE:  
 (B) CLONE: SAC\_24445

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGGGGATCCG CCCACAGCAT TCGGGTATGA GGCAAGGGGA GTGTTCATTC ACACACACAG | 60  |
| TAGCTTCGGG TCTGTGAGGT CTCCTTGTTT CCGGGTAGGT TTCTAAAGAC GGAGAAAAAA | 120 |



ATGATTCTGG TTATCAAGAC TACTGTGACC GTATTAGATC CCAGAATGGG CAAGCATCAG 180  
TGTGTGACCA TCGAACAAA AGGAATTTTT 210

(2) INFORMATION FOR SEQ ID NO:110:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 200 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: SAC\_24527

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGGGGATCCG CCCACCATGG TCTCACTCAG AGACGGGTTT GGTCAGTTTT AAGATGAACT 60  
CCTTCGGATG TAGTGTCCTT AAGTCCTTAT TATCGCTGTC CATCAATTCA CGATAGGATA 120  
GCTGGCTGCG GTGGCAAGTC CGCAGTGGTT GTTCCACCTG CCCACATTAT TCTCTCGTGG 180  
CCATGGTTCT TCCCTTAGAG 200

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 400 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: SAC\_24540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GGGGGATCCG CCCACAGTGG GAAGGATGGA AATAGCTGTC ATCTCTCCAA AACTGAGTTC 60  
CTTTCCTTCA TGAACACGGA GCTGGCCGCC TTCACGAAGA ACCAGAAGGA CCCCGGTGTC 120  
CTCGACCGCA TGATGAAGAA GCTGGACCTC AACAGTGATG GGCAGCTAGA TTTCCAAGAG 180  
TTTCTCAACC TTATTGGTGG CTTAGCTATA GCACCTGCCC ACTCTCGTGG CTGGCCCTCT 240  
GCTTATACTC CTTGGACTGC TCCAGGCTGT GTGTTTCCAC GCTTGACCTG CCCACAGAGC 300  
CAAAAGAGAC ACATTGGCTA CTTTAACCAC CTTAAAGCGG ACTCCAGGAA TATCACCAC 360

GGCATGGCCT TTTGCGAACA AATCCCANCA ACCAAAAAAA

400

## (2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 200 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: SAC\_24623

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GGGGGATCCG CCCACAGTGC ATATTGGCGG CGCTCGCCTC ATTACGATTC GCCAGCTTGC | 60  |
| TTCTCTTGTT CAATTGTTTC TTTTGAAGGC AGAGGATTTT TCTCTTGTTT TTCTGTCTTC | 120 |
| TTCAACTTCG ACTTATCGAA TTTCACCTGC CCACTAAACC CACAGCCCAG CCCTCCTTCC | 180 |
| TTCTCCTGT CCTGGAATTG                                              | 200 |

What is claimed is:

1. Purified and isolated nucleic acid encoding all or a unique fragment of a KIM.
2. Nucleic acid of claim 1 that is RNA.
3. Nucleic acid of claim 1 that is DNA.
- 5 4. Nucleic acid of claim 3 that is cDNA.
5. Nucleic acid that is complementary to the nucleic acid of claim 1.
6. Nucleic acid that hybridizes to the nucleic acid of claim 1 or 5.
7. Nucleic acid of claim 1 that is in operative association with an expression control element therefor.
- 10 8. Antisense nucleic acid of claim 1 that is sufficient, when internalized within a cell, to disrupt expression of a cellular KIM gene.
9. Purified and isolated nucleic acid encoding all or a unique fragment of a KIM, said nucleic acid having a sequence selected from the sequences listed in TABLE 1.
10. Purified and isolated nucleic acid encoding all or a unique fragment of a KIM, said  
15 nucleic acid having a sequence selected from degenerate variants of the sequences listed in TABLE 1.
11. Purified and isolated nucleic acid encoding all or a unique fragment of a KIM, said nucleic acid having a sequence selected from homologous variants of the sequences listed in TABLE 1.
- 20 12. Purified and isolated nucleic acid encoding a KIM fusion polypeptide, the sequence of said nucleic acid comprising a KIM sequence selected from the sequences listed in TABLE 1 fused in frame to a sequence encoding a non- KIM polypeptide.
13. Nucleic acid of claim 12 wherein the encoded non-KIM polypeptide is selected from: a secretable leader polypeptide, an immunoglobulin polypeptide, a binding  
25 pair partner, a toxin or toxoid, an enzyme, and a detectable polypeptide.

14. A vector comprising a KIM-encoding nucleic acid of any one of claims 1 to 13.
15. A host cell stably transformed or transfected with a vector of claim 14.
16. A method for producing a KIM polypeptide, comprising the steps of growing a host cell of claim 15 under conditions sufficient for the production of polypeptides of vector origin; and, recovering an expressed KIM polypeptide.
17. A purified and isolated polypeptide comprising all or a unique fragment of a KIM, said polypeptide having a sequence selected from the sequences encoded by nucleic acids listed in TABLE 1.
18. A purified and isolated polypeptide comprising all or a unique fragment of a KIM, said polypeptide having a sequence selected from variants of the sequences encoded by nucleic acids listed in TABLE 1.
19. A polypeptide of claim 18 wherein said variant is a splice variant, truncation variant, or substitution variant of an encoded TABLE 1 sequence.
20. A KIM fusion polypeptide, the sequence of said polypeptide comprising all or a unique fragment of an encoded KIM sequence listed in TABLE 1, fused to a non-KIM polypeptide sequence.
21. A fusion polypeptide of claim 20 wherein the non-KIM polypeptide sequence is selected from: a secretable leader polypeptide sequence, an immunoglobulin polypeptide sequence, a binding pair partner sequence, a toxin or toxoid sequence, an enzyme sequence, and a detectable polypeptide sequence.
22. A conjugate comprising a KIM polypeptide of claim 17, 18 or 19, linked to a detectable moiety, imageable moiety, radiolabeled moiety, or toxin moiety.
23. A KIM fusion polypeptide, the sequence of said polypeptide comprising all or a unique fragment of an encoded KIM sequence selected from nucleic acid sequences listed in TABLE 2, fused to a non-KIM polypeptide sequence.
24. A fusion polypeptide of claim 23 wherein the non-KIM polypeptide sequence is selected from: a secretable leader polypeptide sequence, an immunoglobulin

polypeptide sequence, a binding pair partner sequence, a toxin or toxoid sequence, an enzyme sequence, and a detectable polypeptide sequence.

25. A conjugate comprising a KIM polypeptide of claim 23 or 24, linked to a detectable moiety, imageable moiety, radiolabeled moiety, or toxin moiety.
- 5 26. An antibody that binds selectively to all or a unique fragment of a KIM polypeptide encoded by a nucleic acid sequence listed in TABLE 1.
27. A conjugate comprising an antibody of claim 26, linked to a detectable moiety, imageable moiety, radiolabeled moiety, or toxin moiety.
28. An antibody that binds selectively to all or a unique fragment of a KIM polypeptide  
10 encoded by a nucleic acid sequence listed in TABLE 2.
29. A conjugate comprising an antibody of claim 29, linked to a detectable moiety, imageable moiety, radiolabeled moiety, or toxin moiety.
30. Use in therapy of an antisense KIM nucleic acid of claim 8.
31. Use in therapy of a KIM vector of claim 14.
- 15 32. Use in therapy of a KIM polypeptide of claim 17, 18 or 19.
33. Use in therapy of a KIM fusion protein of claim 20 or 21, or of a KIM conjugate of claim 22.
34. Use in therapy of an antibody of claim 26, or of an antibody conjugate of claim 27.
35. A pharmaceutical composition comprising a physiologically acceptable carrier  
20 having dispersed therein, to a therapeutically effective concentration: a KIM nucleic acid of claim 8; a KIM vector of claim 14; a KIM polypeptide of claim 17, 18 or 19; a KIM fusion protein of claim 20 or 21; a KIM conjugate of claim 22; an anti-KIM antibody of claim 26; or, an anti-KIM antibody conjugate of claim 27.
36. A method for detecting the presence or status of renal injury or of renal disease,  
25 comprising the step of measuring the concentration of a KIM polypeptide in a

sample selected from serum, urine or urine sediment of an individual afflicted with, or at risk of developing, renal injury or an impairment of renal function.

37. A method for detecting the presence or status of an abnormal response to tissue injury or other stimulus, comprising the step of measuring the concentration of a KIM polypeptide in a sample selected from serum, urine or urine sediment of an individual afflicted with, or at risk of developing, an autoimmune response or abnormal tissue growth arising from or affecting renal tissue.
38. A method according to claim 36 or 37, wherein said measuring step involves contacting said sample with an anti-KIM antibody of claim 26 or 28, or with a conjugate of claim 27 or 29.
39. A kit for practice of the method of claim 36 or 37, comprising at least one reagent selected from: the anti-KIM antibody of claim 26; the anti-KIM antibody of claim 28; the conjugate of claim 27; and, the conjugate of claim 29.
40. A method for detecting the presence or status of renal injury or of renal disease, comprising the step of measuring the level of a KIM nucleic acid in a sample selected from serum, urine or urine sediment of an individual afflicted with, or at risk of developing, renal injury or an impairment of renal function.
41. A method for detecting the presence or status of an abnormal response to tissue injury or other stimulus, comprising the step of measuring the level of a KIM nucleic acid in a sample selected from serum, urine or urine sediment of an individual afflicted with, or at risk of developing, an autoimmune response or abnormal tissue growth arising from or affecting renal tissue.
42. A method according to claim 40 or 41, wherein said measuring step involves contacting said sample with a KIM nucleic acid of claim 9, 10 or 11; or with a nucleic acid probe that hybridizes to KIM nucleic acid of claim 9, 10 or 11; or with a nucleic acid having a sequence selected from sequences listed in TABLE 2; or with a nucleic acid probe that hybridizes to a nucleic acid listed in TABLE 2.

43. A kit for practice of the method of claim 40 or 41, comprising at least one reagent selected from: the KIM nucleic acid of claim 9, 10 or 11; or a nucleic acid probe that hybridizes to KIM nucleic acid of claim 9, 10 or 11; or a nucleic acid having a sequence selected from sequences listed in TABLE 2; or a nucleic acid probe that hybridizes to a nucleic acid listed in TABLE 2.
44. A method of imaging cells or tissue expressing or producing a KIM, comprising the steps of contacting the cells or tissue with an imageable KIM-binding reagent; and, imaging an accumulation of the KIM-binding reagent.
45. A method according to claim 44 wherein the cells or tissue are disposed in body tissue of an individual suspected of harboring an imageable locus of KIM expression and/or production.
46. A method of locating a tissue mass abnormally producing or expressing a KIM in an individual suspected of affliction with an abnormal tissue response to injury or other stimulus, comprising the step of: administering an imageable KIM-binding reagent to the individual; and, imaging said tissue mass within the body of the individual.
47. A method according to claim 44 wherein the tissue mass is a tumor arising from or affecting renal tissue of the individual.
48. A method of treating an individual afflicted with, or at risk of developing, a disease or condition contributed to or associated with a dysfunction or dysregulation of a KIM gene or protein, comprising the step of administering to the individual a pharmaceutical composition of claim 35.
49. A method of treating an individual afflicted with, or at risk of developing, a disease or condition beneficially affected by therapeutic administration of a KIM composition of the present invention, comprising the step of administering to the individual a pharmaceutical composition of claim 35.

50. A method according to claim 48 or 49 wherein the disease is a renal disease; or, the condition is an impairment of renal function.
51. A method of inhibiting the growth of KIM-expressing tumor cells, comprising the step of contacting the tumor cells with a pharmaceutical composition comprising  
5 involving the step of contacting the cells with: an antisense KIM nucleic acid of claim 8; a KIM fusion protein of claim 20, 21, 23 or 24; a KIM conjugate of claim 22 or 25; an antibody of claim 26 or 28; or an antibody conjugate of claim 27 or 29.
52. A method according to claim 36, 37, 40, 41, 45, 46, 47, 48, 49, or 50 wherein the individual is a human.



# INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/10547

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/12 C12N15/62 C12N5/10 C12N1/21 C07K14/47  
C07K16/18 C12Q1/68 A61K31/70 A61K38/17 A61K39/395  
A61K48/00 G01N33/577

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C12N C07K C12Q A61K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages                                                                                                                                                                                                                                                                                            | Relevant to claim No. |
|------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------|
| X          | N.H. LEE ET AL.: "Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment"<br>EMBL SEQUENCE DATABASE, 1 October 1995, XP002080245<br>Heidelberg, FRG<br>EST109574 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA clone PRNAT01 3' end, Accession no. H33500;<br>---<br>-/-- | 5,6                   |

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

### \* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

12 October 1998

Date of mailing of the international search report

22/10/1998

Name and mailing address of the ISA

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# INTERNATIONAL SEARCH REPORT

Int. Jonal Application No

PCT/US 98/10547

| C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT |                                                                                                                                                                                                                                                                                                                                                                       |                       |
|------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------|
| Category                                             | Citation of document, with indication, where appropriate, of the relevant passages                                                                                                                                                                                                                                                                                    | Relevant to claim No. |
| X                                                    | N.H. LEE ET AL.: "Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment"<br>EMBL SEQUENCE DATABASE, 1 October 1995, XP002080246<br>Heidelberg, FRG<br>EST111059 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA clone PRNBQ59 5' end; Accession no. H34282;<br>--- | 6                     |
| X                                                    | N.H. LEE ET AL.: "Comparative expressed-sequence-tag analysis of differential gene expression profiles in PC-12 cells before and after nerve growth factor treatment"<br>EMBL SEQUENCE DATABASE, 1 October 1995, XP002080247<br>Heidelberg, FRG<br>EST111810 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA clone RPNCM27 5' end; Accession no. H34674;<br>--- | 6                     |
| A                                                    | US 5 552 313 A (CALVET JAMES P ET AL)<br>3 September 1996<br>see the whole document<br>---                                                                                                                                                                                                                                                                            | 1-52                  |
| A                                                    | WO 95 26732 A (AMUR RESEARCH CORP ;CHASLOW FRED I (US)) 12 October 1995<br>see the whole document<br>---                                                                                                                                                                                                                                                              | 1-52                  |
| A                                                    | BONALDO FATIMA DE M ET AL: "NORMALIZATION AND SUBTRACTION: TWO APPROACHES TO FACILITATE GENE DISCOVERY"<br>GENOME RESEARCH,<br>vol. 6, no. 9, September 1996, pages 791-806, XP002039972<br>see the whole document<br>---                                                                                                                                             | 1-52                  |
| P,X                                                  | WO 97 44460 A (BIOGEN INC ;SANICOLA NADEL MICHELE (US); BONVENTRE JOSEPH V (US);)<br>27 November 1997<br>cited in the application<br>see the whole document<br>---                                                                                                                                                                                                    | 1-8,<br>35-52         |
| P,X                                                  | M. TAKADA ET AL.: "The cytokine-adhesion molecule cascade in ischemia/perfusion injury of the rat kidney. Inhibition by a soluble P-selectin ligand"<br>J. CLIN. INVEST.,<br>vol. 99, no. 11, 1 June 1997, pages 2682-2690, XP002079925<br>ROCKEFELLER UNIVERSITY PRESS, NEW YORK, US<br>see the whole document<br>---                                                | 1-8                   |
|                                                      | -/--                                                                                                                                                                                                                                                                                                                                                                  |                       |

# INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 98/10547

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category | Citation of document, with indication, where appropriate, of the relevant passages                                                                                                                                                                                                                                                                                                                                         | Relevant to claim No. |
|----------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------|
| P,X      | <p>T. ICHIMURA ET AL.: "Kidney injury molecule-1 (KIM-1), a putative epithelial cell adhesion molecule containing a novel immunoglobulin domain, is up-regulated in renal cells after injury"</p> <p>J. BIOL. CHEM.,<br/>vol. 273, no. 7, 13 February 1998, pages 4135-4142, XP002079926</p> <p>AM. SOC. BIOCHEM.<br/>MOL.BIOL.,INC.,BALTIMORE,US<br/>cited in the application<br/>see the whole document</p> <p>-----</p> | 1-8                   |

# INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 98/10547

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:  
Please see Further Information sheet enclosed.
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 98/10547

| Patent document<br>cited in search report | Publication<br>date | Patent family<br>member(s) | Publication<br>date |
|-------------------------------------------|---------------------|----------------------------|---------------------|
| US 5552313 A                              | 03-09-1996          | NONE                       |                     |
| WO 9526732 A                              | 12-10-1995          | AU 2206495 A               | 23-10-1995          |
| WO 9744460 A                              | 27-11-1997          | AU 3567697 A               | 09-12-1997          |